



SEQUENCE LISTING

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Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
REGULATORY PROTEINS

<130> BGI-123CP

<140> US 09/602,874
<141> 2000-06-23

<150> 60/141031
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Val Glu Thr Gln Ala 5																
ttt cag cgc caa aac acc ggc ctc atc gct atg gtt gcc gcc gat gcg 163																
Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met Val Ala Ala Asp Ala 20																
tcg aat ccc ttc ttc ttg gaa att ttc cgg ggc gcg cag cac gcc gca 211																
Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala 35																
agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259																
Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala 50																
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Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly 65																
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Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val 85																
gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att 403																
Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile 100																
ccc agc gtg atg gtg gat aac tac gac ggt gcg ccg aag gct gtg gtg 451																
Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val 115																
cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct 499																
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Ala Gln His Ala	Ala Ser Thr Gln	Gly Tyr Thr Val	Ala Leu Val Asp
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Ala Arg Glu Ser	Ala Ile Lys Ser	Arg Glu Val Leu	Asp Lys Ile Val
50	55	60	
Pro His Ala Asp	Gly Leu Leu Leu	Ala Ala Ser Arg	Met Asp Ser Gly
65	70	75	80
Glu Ile His Lys	Val Ala Arg Glu	Ile Pro Thr Val	Leu Met Ser Arg
85	90	95	
Glu Val Gln Gly	Ile Pro Ser Val	Met Val Asp Asn	Tyr Asp Gly Ala
100	105	110	
Pro Lys Ala Val	Val His Leu Val	Asp Gln Gly Cys	Arg Ser Ile Thr
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Tyr Ile Ala Gly	Pro Asn Lys Ser	Trp Ala	
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 Val Glu Thr Gln Ala
 1 5
 ttt cag cgc caa aac acc ggc ctc atc gct atg gtt gcc gcc gat gcg 163
 Phe Gln Arg Gln Asn Thr Gly Leu Ile Ala Met Val Ala Ala Asp Ala
 10 15 20
 tcg aat ccc ttc ttc ttg gaa att ttc cgg ggc gcg cag cac gcc gca 211
 Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala
 25 30 35
 agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259
 Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala
 40 45 50
 att aag tcc agg gag gtg ctg gac aag atc gtc ccc cac gcc gat ggc 307
 Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly
 55 60 65
 tta ttg ctc gct gct tca agg atg gat tct ggt gag atc cac aaa gtc 355

Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val
 70 75 80 85
 gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att 403
 Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile
 90 95 100
 ccc agc gtg atg gtg gat aac tac gac ggt gcg ccg aag gct gtg gtg 451
 Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val
 105 110 115
 cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct 499
 His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr Tyr Ile Ala Gly Pro
 120 125 130
 aat aaa tcc tgg gct 514
 Asn Lys Ser Trp Ala
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 Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp
 35 40 45
 Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val
 50 55 60
 Pro His Ala Asp Gly Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly
 65 70 75 80
 Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg
 85 90 95
 Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala
 100 105 110
 Pro Lys Ala Val Val His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr
 115 120 125
 Tyr Ile Ala Gly Pro Asn Lys Ser Trp Ala
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<222> (101)..(553)

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                                         Met Lys Leu Asp Ser
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att gat cgc gca att att gcg gag ctt agc gcg aat gcg cgc atc tca 163
Ile Asp Arg Ala Ile Ile Ala Glu Leu Ser Ala Asn Ala Arg Ile Ser
                        10                        15                        20

aat ctc gca ctg gct gac aag gtg cat ctc act ccg gga cct tgc ttg 211
Asn Leu Ala Leu Ala Asp Lys Val His Leu Thr Pro Gly Pro Cys Leu
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agg agg gtg cag cgt ttg gaa gcc gaa gga atc att ttg ggc tac agc 259
Arg Arg Val Gln Arg Leu Glu Ala Glu Gly Ile Ile Leu Gly Tyr Ser
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gcg gac att cac cct gcg gtg atg aat cgt gga ttt gag gtg acc gtg 307
Ala Asp Ile His Pro Ala Val Met Asn Arg Gly Phe Glu Val Thr Val
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gat gtc act ctc agc aac ttc gac cgc tcc act gta gac aat ttt gaa 355
Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr Val Asp Asn Phe Glu
                        70                        75                        80                        85

agc tcc gtt gcg cag cat gat gaa gta ctg gag ttg cac agg ctt ttt 403
Ser Ser Val Ala Gln His Asp Glu Val Leu Glu Leu His Arg Leu Phe
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ggg tcg cca gat tat ttt gtc cgc atc ggc gtt gct gat ttg gag gcg 451
Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val Ala Asp Leu Glu Ala
                        105                        110                        115

tat gag caa ttt tta tcc agt cac att caa acc gtg cca gga att gca 499
Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr Val Pro Gly Ile Ala
                        120                        125                        130

aag atc tca tca cgt ttt gct atg aaa gtg gtg aaa cca gct cgc ccc 547
Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val Lys Pro Ala Arg Pro
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Gln Val
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 50 55 60
 Phe Glu Val Thr Val Asp Val Thr Leu Ser Asn Phe Asp Arg Ser Thr
 65 70 75 80
 Val Asp Asn Phe Glu Ser Ser Val Ala Gln His Asp Glu Val Leu Glu
 85 90 95
 Leu His Arg Leu Phe Gly Ser Pro Asp Tyr Phe Val Arg Ile Gly Val
 100 105 110
 Ala Asp Leu Glu Ala Tyr Glu Gln Phe Leu Ser Ser His Ile Gln Thr
 115 120 125
 Val Pro Gly Ile Ala Lys Ile Ser Ser Arg Phe Ala Met Lys Val Val
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 Met Thr Thr Glu Ala
 1 5
 ccc att tgg cca gcc gaa ctc ttc gaa gac ctc gac cgc aac gga cca 163
 Pro Ile Trp Pro Ala Glu Leu Phe Glu Asp Leu Asp Arg Asn Gly Pro
 10 15 20
 atc ccc ctc tac ttc caa gta gcc caa cgc ctc gaa gac ggc atc cgc 211
 Ile Pro Leu Tyr Phe Gln Val Ala Gln Arg Leu Glu Asp Gly Ile Arg
 25 30 35
 agc gga gtc ctc cca ccc gga gca cgc cta gaa aac gag atc tcc gtg 259
 Ser Gly Val Leu Pro Pro Gly Ala Arg Leu Glu Asn Glu Ile Ser Val
 40 45 50
 gcg aaa cac ctc aac gta tcc cgc ccc acc gtc cga cgc gcc atc caa 307
 Ala Lys His Leu Asn Val Ser Arg Pro Thr Val Arg Arg Ala Ile Gln
 55 60 65
 gaa gtc gta gac aaa ggc ctc tta gtt cgc cgc cgc ggt gtt ggc acc 355

Glu Val Val Asp Lys Gly Leu Leu Val Arg Arg Arg Gly Val Gly Thr
 70 75 80 85
 cag gtc gtc caa agc cac gtc acc cgc cca gtc gaa ctg acc agt ttc 403
 Gln Val Val Gln Ser His Val Thr Arg Pro Val Glu Leu Thr Ser Phe
 90 95 100
 ttc aac gac ctc aaa aac gcc aac ctg gac ccc aaa acc cga gtc ctc 451
 Phe Asn Asp Leu Lys Asn Ala Asn Leu Asp Pro Lys Thr Arg Val Leu
 105 110 115
 gag cac cgc tcc ttg cag caa gtt ccg cca tcg cag aaa aac tcg gag 499
 Glu His Arg Ser Leu Gln Gln Val Pro Pro Ser Gln Lys Asn Ser Glu
 120 125 130
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 35 40 45
 Asn Glu Ile Ser Val Ala Lys His Leu Asn Val Ser Arg Pro Thr Val
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 Arg Arg Ala Ile Gln Glu Val Val Asp Lys Gly Leu Leu Val Arg Arg
 65 70 75 80
 Arg Gly Val Gly Thr Gln Val Val Gln Ser His Val Thr Arg Pro Val
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 Glu Leu Thr Ser Phe Phe Asn Asp Leu Lys Asn Ala Asn Leu Asp Pro
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 Lys Thr Arg Val Leu Glu His Arg Ser Leu Gln Gln Val Pro Pro Ser
 115 120 125
 Gln Lys Asn Ser Glu Phe Pro Gln Val Thr Lys Ser Ser Ser Ser Ala
 130 135 140
 Ala Ser Ala Pro Pro Glu Thr Ser Pro
 145 150

1	5	10	15
Pro Val Glu Ala Leu Ala Glu Val Val Asp Ala Tyr Pro Gln Leu Ala	20	25	30
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Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala	50	55	60
Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly	65	70	75
Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr	85	90	95
Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly	100	105	110
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 Val Glu Ile Arg Trp
 1 5
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 Ala Ile Arg Leu Gly Met Pro Gln Ser Pro Leu Ser Gln Leu Ile Arg
 25 30 35
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 Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe Asp Arg Ser Thr Arg
 40 45 50
 tcg gtg gag tta act gcc gcg ggt cgg gcg ttt ttg cca cat gcc agg 307
 Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe Leu Pro His Ala Arg
 55 60 65
 ggg att gtg gcg agc gct gcg gtg gcg agg gaa gct gtg aat gct gcc 355

Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu Ala Val Asn Ala Ala
 70 75 80 85
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 Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly Phe Ser Gly Val Leu
 90 95 100
 aac tat tcc acg ctg ccg ctt ttg acc agt gag gtg cat aaa cgg ctt 451
 Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu Val His Lys Arg Leu
 105 110 115
 cct aat gtg gag ttg gag ctg gtt ggt cag aag ttg acg agg gaa gcg 499
 Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys Leu Thr Arg Glu Ala
 120 125 130
 gta agt ttg ctg cgc ttg ggg gcg ttg gat att acg ttg atg ggt ttg 547
 Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile Thr Leu Met Gly Leu
 135 140 145
 ccc att gag gat cca gag att gag act cgg ctg att agt ttg gaa gag 595
 Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu Ile Ser Leu Glu Glu
 150 155 160 165
 ttt tgc gtg gtg ttg ccg aag gat cat cgt ctt gcg ggg gaa gga gtg 643
 Phe Cys Val Val Leu Pro Lys Asp His Arg Leu Ala Gly Glu Gly Val
 170 175 180
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 Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe Val Thr Thr Pro Glu
 185 190 195
 ttt gcg ggg tct gtg ttt agg aat tcc acc ttt cag ttg tgt gct gag 739
 Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe Gln Leu Cys Ala Glu
 200 205 210
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 Ala Gly Phe Val Pro Arg Ile Ser Gln Gln Val Asn Asp Pro Tyr Met
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<212> PRT

<213> Corynebacterium glutamicum

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Ser Gln Leu Ile Arg Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe
 35 40 45

Asp Arg Ser Thr Arg Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe
 50 55 60

Leu Pro His Ala Arg Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu
 65 70 75 80
 Ala Val Asn Ala Ala Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly
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 Phe Ser Gly Val Leu Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu
 100 105 110
 Val His Lys Arg Leu Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys
 115 120 125
 Leu Thr Arg Glu Ala Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile
 130 135 140
 Thr Leu Met Gly Leu Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu
 145 150 155 160
 Ile Ser Leu Glu Glu Phe Cys Val Val Leu Pro Lys Asp His Arg Leu
 165 170 175
 Ala Gly Glu Gly Val Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe
 180 185 190
 Val Thr Thr Pro Glu Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe
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 <223> RXN02553

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 Met Ala Val Lys Arg
 1 5
 aat gag ttg gaa ccc gag ctg acg tcc aac ccc aac cca tta agc gca 163
 Asn Glu Leu Glu Pro Glu Leu Thr Ser Asn Pro Asn Pro Leu Ser Ala
 10 15 20
 gaa gtg cat cat ttg tat cct gag gaa act cgt ctt gca acg gag atc 211
 Glu Val His His Leu Tyr Pro Glu Glu Thr Arg Leu Ala Thr Glu Ile
 25 30 35
 ctg gaa cgc acc aac aat tgg ctt gct gaa aaa ggg atc cct ccg ctg 259

Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys Gly Ile Pro Pro Leu
 40 45 50
 cca cca gcg gaa gtt gta gcc atc tca tta cac ctg gtt aat gct ggt 307
 Pro Pro Ala Glu Val Val Ala Ile Ser Leu His Leu Val Asn Ala Gly
 55 60 65
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 Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val Met Thr Gly Val Phe
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 Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe Gly Ile Thr Leu Asp
 90 95 100
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 Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr His Met Arg Tyr Phe
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 ttt gtt cgc gtt cac cac gac gga caa ctc aac gac ggc atg tcc gtg 499
 Phe Val Arg Val His His Asp Gly Gln Leu Asn Asp Gly Met Ser Val
 120 125 130
 ctg cgc aac agc cta gaa att tcc cac ccg gat tcg gtg gca tgt gcg 547
 Leu Arg Asn Ser Leu Glu Ile Ser His Pro Asp Ser Val Ala Cys Ala
 135 140 145
 gaa aga ctc agc caa atc ctc agc ctt cga ttg ggt gcc gaa ctt tcc 595
 Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu Gly Ala Glu Leu Ser
 150 155 160 165
 tcc gac gag caa acc tac ctc gcg ctc cat gtc gcg agg ttg gct gaa 643
 Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val Ala Arg Leu Ala Glu
 170 175 180
 gat cga ggt act acc gct gat taacaagtgc taggcgcgaa tct 687
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<210> 14

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30
 Leu Ala Thr Glu Ile Leu Glu Arg Thr Asn Asn Trp Leu Ala Glu Lys
 35 40 45
 Gly Ile Pro Pro Leu Pro Pro Ala Glu Val Val Ala Ile Ser Leu His
 50 55 60
 Leu Val Asn Ala Gly Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val
 65 70 75 80

Met Thr Gly Val Phe Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe
85 90 95

Gly Ile Thr Leu Asp Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr
100 105 110

His Met Arg Tyr Phe Phe Val Arg Val His His Asp Gly Gln Leu Asn
115 120 125

Asp Gly Met Ser Val Leu Arg Asn Ser Leu Glu Ile Ser His Pro Asp
130 135 140

Ser Val Ala Cys Ala Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu
145 150 155 160

Gly Ala Glu Leu Ser Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val
165 170 175

Ala Arg Leu Ala Glu Asp Arg Gly Thr Thr Ala Asp
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<222> (101)..(904)

<223> RXS00686

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Met Ala Gly Gly Asn
1 5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
10 15 20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
25 30 35

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
40 45 50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu

90										95					100					
act	gcg	cag	cta	gtg	gtc	cgc	gat	aaa	gat	gaa	gca	ctt	ttg	att	gac	451				
Thr	Ala	Gln	Leu	Val	Val	Arg	Asp	Lys	Asp	Glu	Ala	Leu	Leu	Ile	Asp					
			105						110				115							
cga	gcc	tac	ggc	acg	aag	aaa	att	cca	cgc	tcg	gct	cga	gtc	ggg	ggg	499				
Arg	Ala	Tyr	Gly	Thr	Lys	Lys	Ile	Pro	Arg	Ser	Ala	Arg	Val	Gly	Gly					
		120					125					130								
cga	cta	cct	ctg	aac	tcc	act	gcg	gtt	ggc	aag	att	ctc	ctt	gcg	ttt	547				
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Ser	Thr	Pro	Lys	Thr	Ile	Val	Asn	Pro	Asp	Val	Leu	Ala	Ala	Gln	Leu					
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aaa	caa	att	cac	tcg	caa	ggc	ttt	gcc	atc	aca	cat	gac	gag	caa	cga	691				
Lys	Gln	Ile	His	Ser	Gln	Gly	Phe	Ala	Ile	Thr	His	Asp	Glu	Gln	Arg					
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atc	ggc	ggc	gca	tcg	atc	gcc	gta	ccg	gtc	tgg	cat	aca	gga	aaa	ctg	739				
Ile	Gly	Gly	Ala	Ser	Ile	Ala	Val	Pro	Val	Trp	His	Thr	Gly	Lys	Leu					
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gga	gca	gca	ctg	ggg	ttg	gtg	gtt	ccc	acc	gca	cag	gct	gca	aat	ctt	787				
Gly	Ala	Ala	Leu	Gly	Leu	Val	Pro	Thr	Ala	Gln	Ala	Ala	Ala	Asn	Leu					
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gag	cgc	tat	ctc	ccg	atc	ctt	cag	gcg	aca	agt	cag	aga	att	aca	aaa	835				
Glu	Arg	Tyr	Leu	Pro	Ile	Leu	Gln	Ala	Thr	Ser	Gln	Arg	Ile	Thr	Lys					
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Ala	Thr	Ala	Leu	Ile	Pro	Leu	Asp	Thr	Leu	Leu	Ala	Ser	His	Lys	Asn					
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gca	gaa	cga	aaa	ggc	gat	acc	taa	acccgcc	ctccatctgc	ata						927				
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 Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
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 Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
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 Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125
 Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140
 Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
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 Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
 165 170 175
 Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
 180 185 190
 His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
 195 200 205
 His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
 210 215 220
 Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
 225 230 235 240
 Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
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gat gcc ctc ctg cgc act tct ttg gca tcg gca gaa agc gct tta ggc 163
Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
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aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc 211
Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
25 30 35

gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag 259
Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
40 45 50

gtt gtc tcc tcc atc tac atc gtc gag gaa att acc cgt atg ggt gct 307
Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
55 60 65

ctg gca atg cac gtg gct aat tcc gtg cgc cgc cgt tac ccc gat ccg 355
Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
70 75 80 85

gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc 403
Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
90 95 100

gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa 451
Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
105 110 115

cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat 499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
120 125 130

ctg cat cag cac atc atg cgt att ctc acg ctg cgt cct tgg cct cac 547
Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
135 140 145

gac acc aag agc gcg gtt gat ttg acg ctg ctt tcc cgc ttc tac gag 595
Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu Ser Arg Phe Tyr Glu
150 155 160 165

cgt tac gcc gat cac acg gta aac gtg gcc gcc cgt atc att tac ctg 643
Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
170 175 180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa 691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
185 190 195

agg gcc gat gcc gac atg gag aag cgc tgg gcc gag ctg gag cgg cag 739
Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala Glu Leu Glu Arg Gln
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Phe Arg Thr Ser Glu
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<211> 218

<212> PRT

<213> Corynebacterium glutamicum

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Cys Glu Ser Gln Ala Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala
          35           40           45
Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
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Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
          65           70           75           80
Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
          85           90           95
Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
          100          105          110
Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
          115          120          125
Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu
          130          135          140
Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
          145          150          155          160
Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
          165          170          175
Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
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Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala
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Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu
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<223> RXN02493

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                               1           5

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Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu	
25 30 35	
tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att	259
Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile	
40 45 50	
caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc	307
Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val	
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Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg	
70 75 80 85	
tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac	403
Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp	
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Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg	
105 110 115	
ccg ggt agt cgc atc acc gca gtg cag gca gtg gtc aag cct tta acg	499
Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr	
120 125 130	
ctt atc gac gat cgt ttc gtg atc atc tat gcc tcc gac gaa tcc gaa	547
Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu	
135 140 145	
aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc	595
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His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala	
170 175 180	
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Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg Leu Pro Asp Met Glu	
215 220 225	
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Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp

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Arg	Thr	Gly	Asp	Val	Ile	Leu	Ser	Asn	Gly	Arg	Ala	His	Glu	Leu	Gly
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Ile	Val	His	Glu	Arg	Ser	Val	Asp	Gly	Asn	Val	Trp	Arg	Val	Ala	Gln
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Glu	Ala	Phe	Gln	Asp	Gln	Glu	Thr	His	Ser	Leu	Asp	Val	His	Pro	Asp
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Val	Lys	Pro	Leu	Thr	Leu	Ile	Asp	Asp	Arg	Phe	Val	Ile	Ile	Tyr	Ala
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Val	Ala	Asn	Val	Ser	His	Glu	Leu	Lys	Thr	Pro	Val	Gly	Gly	Met	Ala
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Lys	Ser	Val	Pro	Val	Ser	Val	Ser	Gln	Ser	Ile	Arg	Asn	Asp	Val	Val
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Gly	Arg	Val	Phe	Glu	Arg	Phe	Phe	Arg	Val	Asp	Lys	Ala	Arg	Ser	Arg
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Gln	Thr	Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Val	Lys	His	Val	Met
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Ala	Asn	His	Gly	Gly	Ser	Ile	Ser	Leu	Trp	Ser	Arg	Pro	Gly	Thr	Gly
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Ser	Thr	Phe	Thr	Leu	Glu	Leu	Pro	Val	Tyr	His	Pro	Glu	Ser	Lys	Glu
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<212> DNA

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<222> (101)..(1339)

<223> FRXA02493

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 Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp
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 Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg
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 Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr
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His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala	
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Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser	
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Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala Ile Glu Arg Thr Gln	
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Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile Arg Gly Asp Arg Thr	
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gaa ctc cct gta tac cac cca gag tcc aag gaa ccg gca gga tct aag	1267
Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu Pro Ala Gly Ser Lys	
375 380 385	
cag gga cct agt ttg gat tca cct att cgt acg act gcg tcc aaa gca	1315

Gln Gly Pro Ser Leu Asp Ser Pro Ile Arg Thr Thr Ala Ser Lys Ala
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 35 40 45

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 65 70 75 80

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Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp
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 115 120 125

Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala
 130 135 140

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Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala
 165 170 175

Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val
 180 185 190

Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp
 195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg
 210 215 220

Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala
 225 230 235 240

Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile
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Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu
 260 265 270
 Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro
 275 280 285
 Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val
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 Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln
 305 310 315 320
 Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg
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 Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met
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 Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly
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 Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu
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 <223> RXN00631

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 Val Ala Ala Leu Asp Asp Glu Asn Gln Glu Val Gly Val Lys Lys Glu
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 gca gaa aaa gaa cct gaa ata ggt ccc atc aga gct gcc gga cga gcc 211
 Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg Ala Ala Gly Arg Ala
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 ata ccg ctg cgc acc cgc atc att ttg atc gtg gtg ggt atc gcc ggg 259
 Ile Pro Leu Arg Thr Arg Ile Ile Leu Ile Val Val Gly Ile Ala Gly
 40 45 50

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Leu Gly Leu Leu Val Asn Ala Ile Ala Val Ser Ser Leu Met Arg Glu	
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Val Ser Tyr Thr Arg Met Asp Gln Glu Leu Glu Thr Ser Met Gly Thr	
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Trp Ala His Asn Val Glu Leu Phe Asn Phe Asp Gly Val Arg Gln Gly	
90 95 100	
cca ccc agc gat tat tat gtg gcc aag gtt ttt cct gat gga tcc agc	451
Pro Pro Ser Asp Tyr Tyr Val Ala Lys Val Phe Pro Asp Gly Ser Ser	
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atc atc ttc aac gat gca caa tcg gca ccc gat cta gct gaa acc acc	499
Ile Ile Phe Asn Asp Ala Gln Ser Ala Pro Asp Leu Ala Glu Thr Thr	
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atc ggt act ggt cca cac act gtg gat gct gct agc ggt tct gcc tcc	547
Ile Gly Thr Gly Pro His Thr Val Asp Ala Ala Ser Gly Ser Ala Ser	
135 140 145	
aac act ccg tgg cgt gtg atg gcg gaa aag aac ggt gac att atc acc	595
Asn Thr Pro Trp Arg Val Met Ala Glu Lys Asn Gly Asp Ile Ile Thr	
150 155 160 165	
gtg gtg ggt aaa agc atg ggg cgt gaa aca aac ctg ctg tac cga ttg	643
Val Val Gly Lys Ser Met Gly Arg Glu Thr Asn Leu Leu Tyr Arg Leu	
170 175 180	
gtg atg gtg cag atg atc atc ggc gcg ctg att ctg gtt gct att ttg	691
Val Met Val Gln Met Ile Ile Gly Ala Leu Ile Leu Val Ala Ile Leu	
185 190 195	
att act tca ctc ttc cta gtc aga cgc tcg ttg cgg ccg ttg aga gaa	739
Ile Thr Ser Leu Phe Leu Val Arg Arg Ser Leu Arg Pro Leu Arg Glu	
200 205 210	
ggt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt	787
Val Glu Glu Thr Ala Thr Arg Ile Ala Gly Gly Asp Leu Asp Arg Arg	
215 220 225	
gtc ccg cag tgg cca atg acc aca gaa gtc gga cag ctg tcg aat gcc	835
Val Pro Gln Trp Pro Met Thr Thr Glu Val Gly Gln Leu Ser Asn Ala	
230 235 240 245	
ctc aat atc atg ttg gag cag ctc caa gcc tca att ctg acc gcc cag	883
Leu Asn Ile Met Leu Glu Gln Leu Gln Ala Ser Ile Leu Thr Ala Gln	
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caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag	931
Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu	
265 270 275	
ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca	979
Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser	
280 285 290	
tca ggt gca aca gat gat gcc aac tgg gtc atg tcc aag atc ggt ggc	1027

Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
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gaa gcc caa cgc atg agt gtg ctt gtg gaa gac ctc ctg tca ctg acg 1075
 Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp Leu Leu Ser Leu Thr
 310 315 320 325

cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa 1123
 Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
 330 335 340

ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc 1171
 Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
 345 350 355

aca gtc aat gta tcc aac aaa gct gag tcc att ccg gtt gtc aaa ggc 1219
 Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
 360 365 370

gac cca act cgc ctc cac caa gtg ctt acc aac ctg gtt gcc aac gga 1267
 Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
 375 380 385

cta aac cac ggc gga ccg gac gcg gaa gtc agc att gag atc aac acc 1315
 Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
 390 395 400 405

gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg 1363
 Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
 410 415 420

tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat 1411
 Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
 425 430 435

tcc tcc cgc tca cgc gca tcc ggc gga tcg ggc ctc ggc ctt gcg atc 1459
 Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
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acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc 1507
 Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
 455 460 465

gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg ccg gcg gtt tct 1555
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<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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Gly Val Lys Lys Glu Ala Glu Lys Glu Pro Glu Ile Gly Pro Ile Arg
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Thr	Ser	Met	Gly	Thr	Trp	Ala	His	Asn	Val	Glu	Leu	Phe	Asn	Phe	Asp
				85					90					95	
Gly	Val	Arg	Gln	Gly	Pro	Pro	Ser	Asp	Tyr	Tyr	Val	Ala	Lys	Val	Phe
			100					105					110		
Pro	Asp	Gly	Ser	Ser	Ile	Ile	Phe	Asn	Asp	Ala	Gln	Ser	Ala	Pro	Asp
		115					120					125			
Leu	Ala	Glu	Thr	Thr	Ile	Gly	Thr	Gly	Pro	His	Thr	Val	Asp	Ala	Ala
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Ser	Gly	Ser	Ala	Ser	Asn	Thr	Pro	Trp	Arg	Val	Met	Ala	Glu	Lys	Asn
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Gly	Asp	Ile	Ile	Thr	Val	Val	Gly	Lys	Ser	Met	Gly	Arg	Glu	Thr	Asn
				165					170					175	
Leu	Leu	Tyr	Arg	Leu	Val	Met	Val	Gln	Met	Ile	Ile	Gly	Ala	Leu	Ile
			180					185					190		
Leu	Val	Ala	Ile	Leu	Ile	Thr	Ser	Leu	Phe	Leu	Val	Arg	Arg	Ser	Leu
		195					200					205			
Arg	Pro	Leu	Arg	Glu	Val	Glu	Glu	Thr	Ala	Thr	Arg	Ile	Ala	Gly	Gly
	210					215					220				
Asp	Leu	Asp	Arg	Arg	Val	Pro	Gln	Trp	Pro	Met	Thr	Thr	Glu	Val	Gly
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Gln	Leu	Ser	Asn	Ala	Leu	Asn	Ile	Met	Leu	Glu	Gln	Leu	Gln	Ala	Ser
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Ile	Leu	Thr	Ala	Gln	Gln	Lys	Glu	Ala	Gln	Met	Arg	Arg	Phe	Val	Gly
			260					265					270		
Asp	Ala	Ser	His	Glu	Leu	Arg	Thr	Pro	Leu	Thr	Ser	Val	Lys	Gly	Phe
	275						280					285			
Thr	Glu	Leu	Tyr	Ser	Ser	Gly	Ala	Thr	Asp	Asp	Ala	Asn	Trp	Val	Met
	290					295					300				
Ser	Lys	Ile	Gly	Gly	Glu	Ala	Gln	Arg	Met	Ser	Val	Leu	Val	Glu	Asp
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Leu	Leu	Ser	Leu	Thr	Arg	Ala	Glu	Gly	Gln	Gln	Met	Glu	Lys	His	Arg
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Val	Asp	Val	Leu	Glu	Leu	Ala	Leu	Ala	Val	Arg	Gly	Ser	Met	Arg	Ala
			340					345					350		

Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
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Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
 370 375 380

Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
 385 390 395 400

Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
 405 410 415

Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
 420 425 430

Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly
 435 440 445

Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
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Val Thr Val Asp Ser Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr
 465 470 475 480

Leu Pro Ala Val Ser
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<210> 25
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (12)..(1583)
 <223> RXN00291

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 Ile Phe Ala Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His
 15 20 25

aca gcg ctg tcc atc gga cgt tgg gtg gca tcc aac ccg cag atc cgc 146
 Thr Ala Leu Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg
 30 35 40 45

gag gaa gta gcg ctt gat act caa aca gga gca aac cca tcg gcc gaa 194
 Glu Glu Val Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu
 50 55 60

gaa tta gcc gat gga gat atc caa gcg gtt gca cag gcg gcc aat gaa 242
 Glu Leu Ala Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu
 65 70 75

cgc act gga gct ttg ttt gtc gtt atc act gac ggt tta ggt atc cgc 290
 Arg Thr Gly Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg

80	85	90	
ctg tcc cac cca gat gag gaa cgt ctg ggg gag cag gtg agc act agc Leu Ser His Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser 95 100 105			338
ttt gag gct gcc atg cgg ggt gaa gaa acc atg gcg tgg gag act ggg Phe Glu Ala Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly 110 115 120 125			386
acc ctc ggt gcg tcc gcg cga gca aaa gtg cct atc ttt gcg ccg gat Thr Leu Gly Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp 130 135 140			434
tct agt gtt cca gtc ggt gag gtc agt gtt ggg ttt gag cga gac agt Ser Ser Val Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser 145 150 155			482
gtg tat tcc cgc ctg ccc atg ttc ctc gcc gcc ctt gct ctt att tct Val Tyr Ser Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser 160 165 170			530
gtg ttg gga atc ctt atc ggc gtg ggt gta gcc atg ggc atg cga cgc Val Leu Gly Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg 175 180 185			578
cgt tgg gaa cgc gtg acc ttg ggt ttg cag ccg gag gag cta gtg acc Arg Trp Glu Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr 190 195 200 205			626
ctt gtg caa aat cag act gca gtc atc gat ggc att gat gag ggc gtg Leu Val Gln Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val 210 215 220			674
ctg gcg ctg agc cca aac gga aca att ggg gtg cat aat gag cag gcg Leu Ala Leu Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala 225 230 235			722
caa tcc atg att ggt gca ggt cct atg agt ggc agg acg ttg aaa gaa Gln Ser Met Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu 240 245 250			770
cta ggg ctt gac ctg ggt ctt gat ggc gtt gta ttg cat ggt cag cat Leu Gly Leu Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His 255 260 265			818
ccg gaa acc gtt gcc cat aac ggc agg atc ctc tat ctg gat ttc cac Pro Glu Thr Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His 270 275 280 285			866
ccc gtg cgc cgt ggg gat caa gat tta ggc tac gtg gta acc atc cgc Pro Val Arg Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg 290 295 300			914
gat cgt acc gac atc att gaa ctc agt gaa cgc ctc gac tct gtg cgc Asp Arg Thr Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg 305 310 315			962
acc atg acc cac gca ctc cgc gcc cag cgc cac gag ttt gcc aac cgc Thr Met Thr His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg 320 325 330			1010

atc cac acc gca aca ggg ctt atc gac gcc ggc cgc gtc cac gac gcg 1058
 Ile His Thr Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala
 335 340 345

gca gag ttt cta ggc gat ata tcc cgc aac ggg gga cag tca cat cca 1106
 Ala Glu Phe Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro
 350 355 360 365

ttg atc gga tca gcg cac ctc aat gaa gca ttt ttg agc tca ttt tta 1154
 Leu Ile Gly Ser Ala His Leu Asn Glu Ala Phe Leu Ser Ser Phe Leu
 370 375 380

agt act gct tct att tcg gca tct gaa aag ggc gtt agt ctg cgc atc 1202
 Ser Thr Ala Ser Ile Ser Ala Ser Glu Lys Gly Val Ser Leu Arg Ile
 385 390 395

aac tct gac acg ctc atc ctt ggc act gtt aaa gat cca gaa gat gta 1250
 Asn Ser Asp Thr Leu Ile Leu Gly Thr Val Lys Asp Pro Glu Asp Val
 400 405 410

gca acc att ttg ggt aat tta atc aac aat gcc atc gac gcc gcg gtg 1298
 Ala Thr Ile Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val
 415 420 425

gca ggt gaa gcc cca cgg tgg att gag ctt acg ttg atg gat gat gcc 1346
 Ala Gly Glu Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala
 430 435 440 445

gat acg ctg gtc att tct gtt gca gat tct ggt cct gga atc cca gag 1394
 Asp Thr Leu Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu
 450 455 460

ggc gtg gat gta ttt gcc aca gcc acc cag ata gga gac tct gaa gat 1442
 Gly Val Asp Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp
 465 470 475

aat gaa cgc acc cac ggg cat ggc att ggt cta aaa ctg tgc cgg gct 1490
 Asn Glu Arg Thr His Gly His Gly Ile Gly Leu Lys Leu Cys Arg Ala
 480 485 490

ttg gct aga tca cat ggt ggc gat gtc tgg gtg att gat aga gga acc 1538
 Leu Ala Arg Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr
 495 500 505

gaa gat ggc gct gta ttt gga gtg aaa cta ccg gga gta atg gag 1583
 Glu Asp Gly Ala Val Phe Gly Val Lys Leu Pro Gly Val Met Glu
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<211> 524

<212> PRT

<213> Corynebacterium glutamicum

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 Ser Ile Gly Arg Trp Val Ala Ser Asn Pro Gln Ile Arg Glu Glu Val
 35 40 45
 Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala
 50 55 60
 Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly
 65 70 75 80
 Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His
 85 90 95
 Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala
 100 105 110
 Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly
 115 120 125
 Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val
 130 135 140
 Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser
 145 150 155 160
 Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly
 165 170 175
 Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu
 180 185 190
 Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln
 195 200 205
 Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu
 210 215 220
 Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala Gln Ser Met
 225 230 235 240
 Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu
 245 250 255
 Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His Pro Glu Thr
 260 265 270
 Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His Pro Val Arg
 275 280 285
 Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg Asp Arg Thr
 290 295 300
 Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg Thr Met Thr
 305 310 315 320
 His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg Ile His Thr
 325 330 335
 Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala Ala Glu Phe

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		355					360					365			
Ser	Ala	His	Leu	Asn	Glu	Ala	Phe	Leu	Ser	Ser	Phe	Leu	Ser	Thr	Ala
	370					375					380				
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385					390					395					400
Thr	Leu	Ile	Leu	Gly	Thr	Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile
				405					410					415	
Leu	Gly	Asn	Leu	Ile	Asn	Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Gly	Glu
		420						425					430		
Ala	Pro	Arg	Trp	Ile	Glu	Leu	Thr	Leu	Met	Asp	Asp	Ala	Asp	Thr	Leu
		435					440					445			
Val	Ile	Ser	Val	Ala	Asp	Ser	Gly	Pro	Gly	Ile	Pro	Glu	Gly	Val	Asp
	450					455					460				
Val	Phe	Ala	Thr	Ala	Thr	Gln	Ile	Gly	Asp	Ser	Glu	Asp	Asn	Glu	Arg
465					470					475					480
Thr	His	Gly	His	Gly	Ile	Gly	Leu	Lys	Leu	Cys	Arg	Ala	Leu	Ala	Arg
				485					490					495	
Ser	His	Gly	Gly	Asp	Val	Trp	Val	Ile	Asp	Arg	Gly	Thr	Glu	Asp	Gly
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 <222> (1)..(1074)
 <223> FRXA00291

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1				5					10					15		
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Val	Ala	Met	Gly	Met	Arg	Arg	Arg	Trp	Glu	Arg	Val	Thr	Leu	Gly	Leu	
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cag ccg gag gag cta gtg acc ctt gtg caa aat cag act gca gtc atc															144	
Gln	Pro	Glu	Glu	Leu	Val	Thr	Leu	Val	Gln	Asn	Gln	Thr	Ala	Val	Ile	
		35					40					45				
gat ggc att gat gag ggc gtg ctg gcg ctg agc cca aac gga aca att															192	
Asp	Gly	Ile	Asp	Glu	Gly	Val	Leu	Ala	Leu	Ser	Pro	Asn	Gly	Thr	Ile	

50					55					60						
ggg	gtg	cat	aat	gag	cag	gcg	caa	tcc	atg	att	ggt	gca	ggt	cct	atg	240
Gly	Val	His	Asn	Glu	Gln	Ala	Gln	Ser	Met	Ile	Gly	Ala	Gly	Pro	Met	
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agt	ggc	agg	acg	ttg	aaa	gaa	cta	ggg	ctt	gac	ctg	ggt	ctt	gat	ggc	288
Ser	Gly	Arg	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Asp	Leu	Gly	Leu	Asp	Gly	
				85					90					95		
gtt	gta	ttg	cat	ggt	cag	cat	ccg	gaa	acc	gtt	gcc	cat	aac	ggc	agg	336
Val	Val	Leu	His	Gly	Gln	His	Pro	Glu	Thr	Val	Ala	His	Asn	Gly	Arg	
			100					105					110			
atc	ctc	tat	ctg	gat	ttc	cac	ccc	gtg	cgc	cgt	ggg	gat	caa	gat	tta	384
Ile	Leu	Tyr	Leu	Asp	Phe	His	Pro	Val	Arg	Arg	Gly	Asp	Gln	Asp	Leu	
		115					120					125				
ggc	tac	gtg	gta	acc	atc	cgc	gat	cgt	acc	gac	atc	att	gaa	ctc	agt	432
Gly	Tyr	Val	Val	Thr	Ile	Arg	Asp	Arg	Thr	Asp	Ile	Ile	Glu	Leu	Ser	
	130					135					140					
gaa	cgc	ctc	gac	tct	gtg	cgc	acc	atg	acc	cac	gca	ctc	cgc	gcc	cag	480
Glu	Arg	Leu	Asp	Ser	Val	Arg	Thr	Met	Thr	His	Ala	Leu	Arg	Ala	Gln	
145					150					155					160	
cgc	cac	gag	ttt	gcc	aac	cgc	atc	cac	acc	gca	aca	ggg	ctt	atc	gac	528
Arg	His	Glu	Phe	Ala	Asn	Arg	Ile	His	Thr	Ala	Thr	Gly	Leu	Ile	Asp	
				165					170					175		
gcc	ggc	cgc	gtc	cac	gac	gcg	gca	gag	ttt	cta	ggc	gat	ata	tcc	cgc	576
Ala	Gly	Arg	Val	His	Asp	Ala	Ala	Glu	Phe	Leu	Gly	Asp	Ile	Ser	Arg	
			180					185					190			
aac	ggg	gga	cag	tca	cat	cca	ttg	atc	gga	tca	gcg	cac	ctc	aat	gaa	624
Asn	Gly	Gly	Gln	Ser	His	Pro	Leu	Ile	Gly	Ser	Ala	His	Leu	Asn	Glu	
		195					200					205				
gca	ttt	ttg	agc	tca	ttt	tta	agt	act	gct	tct	att	tcg	gca	tct	gaa	672
Ala	Phe	Leu	Ser	Ser	Phe	Leu	Ser	Thr	Ala	Ser	Ile	Ser	Ala	Ser	Glu	
	210					215					220					
aag	ggc	gtt	agt	ctg	cgc	atc	aac	tct	gac	acg	ctc	atc	ctt	ggc	act	720
Lys	Gly	Val	Ser	Leu	Arg	Ile	Asn	Ser	Asp	Thr	Leu	Ile	Leu	Gly	Thr	
225					230				235					240		
gtt	aaa	gat	cca	gaa	gat	gta	gca	acc	att	ttg	ggt	aat	tta	atc	aac	768
Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile	Leu	Gly	Asn	Leu	Ile	Asn	
				245					250					255		
aat	gcc	atc	gac	gcc	gcg	gtg	gca	ggt	gaa	gcc	cca	cgg	tggt	att	gag	816
Asn	Ala	Ile	Asp	Ala	Ala	Val	Ala	Gly	Glu	Ala	Pro	Arg	Trp	Ile	Glu	
			260					265					270			
ctt	acg	ttg	atg	gat	gat	gcc	gat	acg	ctg	gtc	att	tct	gtt	gca	gat	864
Leu	Thr	Leu	Met	Asp	Asp	Ala	Asp	Thr	Leu	Val	Ile	Ser	Val	Ala	Asp	
			275				280					285				
tct	ggt	cct	gga	atc	cca	gag	ggc	gtg	gat	gta	ttt	gcc	aca	gcc	acc	912
Ser	Gly	Pro	Gly	Ile	Pro	Glu	Gly	Val	Asp	Val	Phe	Ala	Thr	Ala	Thr	
	290					295					300					

cag ata gga gac tct gaa gat aat gaa cgc acc cac ggg cat ggc att 960
 Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile
 305 310 315 320
 ggt cta aaa ctg tgc cgg gct ttg gct aga tca cat ggt ggc gat gtc 1008
 Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val
 325 330 335
 tgg gtg att gat aga gga acc gaa gat ggc gct gta ttt gga gtg aaa 1056
 Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val Lys
 340 345 350
 cta ccg gga gta atg gag taatggatca aacacttaaa gtt 1097
 Leu Pro Gly Val Met Glu
 355

<210> 28
 <211> 358
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 28
 Ala Ala Leu Ala Leu Ile Ser Val Leu Gly Ile Leu Ile Gly Val Gly
 1 5 10 15
 Val Ala Met Gly Met Arg Arg Arg Trp Glu Arg Val Thr Leu Gly Leu
 20 25 30
 Gln Pro Glu Glu Leu Val Thr Leu Val Gln Asn Gln Thr Ala Val Ile
 35 40 45
 Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr Ile
 50 55 60
 Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met
 65 70 75 80
 Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly
 85 90 95
 Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg
 100 105 110
 Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu
 115 120 125
 Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser
 130 135 140
 Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln
 145 150 155 160
 Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp
 165 170 175
 Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg
 180 185 190
 Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu

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<210> 29
<211> 1620
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101) .. (1597)
<223> BXA00129
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<400> 29
agttttttcat ttaaaaaagg ggcagtttct cattcttgcc tggctcacgc gacttcgaca 60

tcgcattgta gataaatggc gaacctcact gcagggttcgc gtg ctc ggc tcc atc 115
                                         Val Leu Gly Ser Ile
                                         1                               5

ttc acc gca tca gct gtc gtg atg atc ctt ttg ggg ctg ggc atg ctg 163
Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu Gly Leu Gly Met Leu
                        10                        15                        20

act gta ttc acc caa cgg ttg gtg gat cag aaa atc gat att gcg agc 211
Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys Ile Asp Ile Ala Ser
                        25                        30                        35

tcc gaa atc gac cgc gcc cgc gtc atc gtc gaa gag caa atc acc gca 259
Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu Glu Gln Ile Thr Ala
                        40                        45                        50

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tcc ggc gcc tca aca tcg gtg cag gcg cga gtg aac tct gcc cgc gct	307
Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val Asn Ser Ala Arg Ala	
55 60 65	
gcg ctc tcc agc ttg ggt acc agc ggc ggt aca gaa acc aac gcc gcc	355
Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr Glu Thr Asn Ala Ala	
70 75 80 85	
tac gat cca gtc gtg ttg gtg aac aac gat gac ctg gtg gtc tct ccc	403
Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp Leu Val Val Ser Pro	
90 95 100	
gag ggt tac caa atc cca gaa cgt ctg cga tac ttc gtc tct gag aac	451
Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr Phe Val Ser Glu Asn	
105 110 115	
caa gtc tcg tat cag ttc tcc agc atc gac caa ggc gac gga tcg tcc	499
Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln Gly Asp Gly Ser Ser	
120 125 130	
tac caa gcg ctc atc atc gga acg ccc acg gaa agc gac atc ccg aac	547
Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu Ser Asp Ile Pro Asn	
135 140 145	
ctc cag gtg tat ctg gtg ttc tcc atg gaa agc gac gaa tcc tct ctt	595
Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser Asp Glu Ser Ser Leu	
150 155 160 165	
gct ctc atg cga gga ctc ctc tca gct gca ctg ctg atc gtg gtg gtg	643
Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu Leu Ile Val Val Val	
170 175 180	
ctg ctg gtc ggt atc gca tgg cta gcc acc caa cag gtc acc gcg ccg	691
Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln Gln Val Thr Ala Pro	
185 190 195	
gtg cgt tcg gcg agc cgg att gcg gag cgt ttc gct caa ggc aaa ctg	739
Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe Ala Gln Gly Lys Leu	
200 205 210	
cgt gaa cgc atg gtg gtg gaa ggc gaa gac gag atg gcc cgc ctg gcg	787
Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu Met Ala Arg Leu Ala	
215 220 225	
gtg tcc ttc aac gcg atg gcc gaa tcg ctg tcc gcg cag atc acc aaa	835
Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser Ala Gln Ile Thr Lys	
230 235 240 245	
ttg gag gaa tac ggc aat ctg caa cga caa ttc aca tcg gat gtc tca	883
Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe Thr Ser Asp Val Ser	
250 255 260	
cac gaa ttg cgc aca ccg ctg aca acg gtg cgc atg gct gct gat cta	931
His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg Met Ala Ala Asp Leu	
265 270 275	
att gcc gat agt gaa gat gaa ctt tca ccc ggt gcg cgc cgc gcc agc	979
Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly Ala Arg Arg Ala Ser	
280 285 290	


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caa ctg atg aac agg gag ttg gac cga ttc gag tcg ctg ctg agc gat 1027
Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu Ser Leu Leu Ser Asp
295 300 305

ctg ttg gaa att tcc cga cac gac gcc ggc gtt gcc gaa ctg tcc acc 1075
Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val Ala Glu Leu Ser Thr
310 315 320 325

gcg ctt cac gat gtc cgc atc cca gtg cga tcg gca ttg gaa caa gta 1123
Ala Leu His Asp Val Arg Ile Pro Val Arg Ser Ala Leu Glu Gln Val
330 335 340

caa cac ttg gcc acc gag ctc gat gtg gaa ttg ctt gtt aat ttg ccc 1171
Gln His Leu Ala Thr Glu Leu Asp Val Glu Leu Leu Val Asn Leu Pro
345 350 355

gaa gaa gcg atc aac att caa ggc gat tcc agg cgc atc gaa aga atc 1219
Glu Glu Ala Ile Asn Ile Gln Gly Asp Ser Arg Arg Ile Glu Arg Ile
360 365 370

att cgc aac ctt cta gcc aat gcg atc gac cac tcc aag ggc ttg cct 1267
Ile Arg Asn Leu Leu Ala Asn Ala Ile Asp His Ser Lys Gly Leu Pro
375 380 385

gtt gag ttg aaa gtt gcc gac aac gtg gac gca gta gcg atc gtt gtt 1315
Val Glu Leu Lys Val Ala Asp Asn Val Asp Ala Val Ala Ile Val Val
390 395 400 405

att gat cac ggc gtc ggc ctg aaa cct gga caa gac gaa ttg gtg ttc 1363
Ile Asp His Gly Val Gly Leu Lys Pro Gly Gln Asp Glu Leu Val Phe
410 415 420

aac aga ttc tgg cga gcc gac cct tcg cgc gtc cgc cat tct ggt ggc 1411
Asn Arg Phe Trp Arg Ala Asp Pro Ser Arg Val Arg His Ser Gly Gly
425 430 435

acc ggc ctg ggt ctt gcg att tct cgc gaa gat gcg atg ctt cat gga 1459
Thr Gly Leu Gly Leu Ala Ile Ser Arg Glu Asp Ala Met Leu His Gly
440 445 450

gga aac ctt gat gcg gcg gga acg atc ggt gtt ggt tcc att ttc cgt 1507
Gly Asn Leu Asp Ala Ala Gly Thr Ile Gly Val Gly Ser Ile Phe Arg
455 460 465

ttg gtc ttg cct aaa gaa ccg cat gga aat tat cgt gaa gca ccg atc 1555
Leu Val Leu Pro Lys Glu Pro His Gly Asn Tyr Arg Glu Ala Pro Ile
470 475 480 485

ccg ttg atc gct cca gag aca ccg tgg gaa ggg gag cag cag 1597
Pro Leu Ile Ala Pro Glu Thr Pro Trp Glu Gly Glu Gln Gln
490 495

tgagtaaaat ttcgacgaaa ctg 1620

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<210> 30

<211> 499

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

Val Leu Gly Ser Ile Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu
 1 5 10 15
 Gly Leu Gly Met Leu Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys
 20 25 30
 Ile Asp Ile Ala Ser Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu
 35 40 45
 Glu Gln Ile Thr Ala Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val
 50 55 60
 Asn Ser Ala Arg Ala Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr
 65 70 75 80
 Glu Thr Asn Ala Ala Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp
 85 90 95
 Leu Val Val Ser Pro Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr
 100 105 110
 Phe Val Ser Glu Asn Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln
 115 120 125
 Gly Asp Gly Ser Ser Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu
 130 135 140
 Ser Asp Ile Pro Asn Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser
 145 150 155 160
 Asp Glu Ser Ser Leu Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu
 165 170 175
 Leu Ile Val Val Val Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln
 180 185 190
 Gln Val Thr Ala Pro Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe
 195 200 205
 Ala Gln Gly Lys Leu Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu
 210 215 220
 Met Ala Arg Leu Ala Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser
 225 230 235 240
 Ala Gln Ile Thr Lys Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe
 245 250 255
 Thr Ser Asp Val Ser His Glu Leu Arg Thr Pro Leu Thr Thr Val Arg
 260 265 270
 Met Ala Ala Asp Leu Ile Ala Asp Ser Glu Asp Glu Leu Ser Pro Gly
 275 280 285
 Ala Arg Arg Ala Ser Gln Leu Met Asn Arg Glu Leu Asp Arg Phe Glu
 290 295 300
 Ser Leu Leu Ser Asp Leu Leu Glu Ile Ser Arg His Asp Ala Gly Val
 305 310 315 320
 Ala Glu Leu Ser Thr Ala Leu His Asp Val Arg Ile Pro Val Arg Ser

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<210> 31
<211> 1455
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1432)
<223> RXN00651
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<400> 31
ggctgcctcg gtggtggtct ctgggggttgc ttcaggttcc gccgggggtac aagcggtgag 60
catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115
/ Met Gln Ser Ser Leu
1 5
gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163
Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu
10 15 20
gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211
Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
25 30 35

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cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc	259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala	
40 45 50	
cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg	307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val	
55 60 65	
tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc	355
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser	
70 75 80 85	
cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att	403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile	
90 95 100	
ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg	451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu	
105 110 115	
ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg	499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala	
120 125 130	
att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg	547
Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly	
135 140 145	
ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc	595
Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr	
150 155 160 165	
gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa	643
Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu	
170 175 180	
aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg	691
Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala	
185 190 195	
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg	739
Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala	
200 205 210	
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg	787
His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met	
215 220 225	
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag	835
Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu	
230 235 240 245	
aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca	883
Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr	
250 255 260	
gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa	931
Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Leu Gln	
265 270 275	
ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc	979

Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 280 285 290

aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat 1027
 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
 295 300 305

gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct 1075
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 310 315 320 325

caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc 1123
 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 330 335 340

cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt 1171
 His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val
 345 350 355

gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct 1219
 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
 360 365 370

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 375 380 385

ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 390 395 400 405

gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363
 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
 410 415 420

ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
 425 430 435

agt tct cca act gac gat gag taaggctaga ctaaagtacg att , 1455
 Ser Ser Pro Thr Asp Asp Glu
 440

<210> 32

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu
 1 5 10 15

Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser
 20 25 30

Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly
 35 40 45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
 50 55 60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
 65 70 75 80
 Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
 85 90 95
 Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
 100 105 110
 Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
 115 120 125
 Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
 130 135 140
 Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
 145 150 155 160
 Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
 165 170 175
 Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr
 180 185 190
 Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu
 195 200 205
 Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu
 210 215 220
 Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val
 225 230 235 240
 Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg
 245 250 255
 Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met
 260 265 270
 Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala
 275 280 285
 Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile
 290 295 300
 Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr
 305 310 315 320
 Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser
 325 330 335
 Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val
 340 345 350
 Arg Leu Asp Val Val Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val
 355 360 365
 Ser Ser Thr Pro Ala Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln
 370 375 380

Gln Arg Ala Met Glu Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr
 385 390 395 400

Gly Gln Gly Thr Ala Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu
 405 410 415

Gly Phe Val Gly Ala Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr
 420 425 430

Gly Glu Val Glu Leu Ser Ser Pro Thr Asp Asp Glu
 435 440

<210> 33
 <211> 1455
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1432)
 <223> FRXA00651

<400> 33
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catgatggaa gcagcgagga tagtaggtaa tgtacgacgc atg cag tca agc cta 115
 Met Gln Ser Ser Leu
 1 5

gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt 163
 Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu
 10 15 20

gtg aag aag ggg aat caa ccg ggc gcg atg agc tat cgc aac agt atc 211
 Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile
 25 30 35

cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc 259
 His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala
 40 45 50

cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg 307
 Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val
 55 60 65

tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc 355
 Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
 70 75 80 85

cac ggc atg cag ctg ggc tgg ctg ttt gtg ctg acg ctg gtg tgg att 403
 His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
 90 95 100

ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg 451
 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
 105 110 115

ttt ttc ctc tat cta cag gtg atg cct gac gtg aga ggc att att gcg 499
 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 120 125 130

att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly 135 140 145	547
ttg acc ttt ggt ggt gtg atg ggt ccg gtg gtc tct gcg atc gtg acc Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr 150 155 160 165	595
gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu 170 175 180	643
aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala 185 190 195	691
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala 200 205 210	739
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met 215 220 225	787
ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu 230 235 240 245	835
aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr 250 255 260	883
gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Ala Leu Gln 265 270 275	931
ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val 280 285 290	979
aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp 295 300 305	1027
gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala 310 315 320 325	1075
caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys 330 335 340	1123
cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val 345 350 355	1171
gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala 360 365 370	1219

ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 375 380 385

 ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 390 395 400 405

 gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363
 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
 410 415 420

 ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
 425 430 435

 agt tct cca act gac gat gag taaggctaga ctaaagtacg att 1455
 Ser Ser Pro Thr Asp Asp Glu
 440

<210> 34
 <211> 444
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 34
 Met Gln Ser Ser Leu Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu
 1 5 10 15

 Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser
 20 25 30

 Tyr Arg Asn Ser Ile His Ile Leu Thr Ala Ser Leu Leu Val Val Gly
 35 40 45

 Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
 50 55 60

 Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
 65 70 75 80

 Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
 85 90 95

 Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
 100 105 110

 Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
 115 120 125

 Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
 130 135 140

 Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
 145 150 155 160

 Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
 165 170 175

 Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr

180					185					190					
Arg	Ser	Gln	Leu	Ala	Val	Thr	Glu	Arg	Asn	Ala	Gly	Ile	Ala	Ala	Glu
		195					200					205			
Arg	Gln	Arg	Ile	Ala	His	Glu	Ile	His	Asp	Thr	Val	Ala	Gln	Gly	Leu
	210					215					220				
Ser	Ser	Ile	Gln	Met	Leu	Leu	His	Val	Ser	Glu	Gln	Glu	Ile	Leu	Val
225					230					235					240
Ala	Glu	Met	Glu	Glu	Lys	Pro	Lys	Glu	Ala	Ile	Val	Lys	Lys	Met	Arg
				245					250					255	
Leu	Ala	Arg	Gln	Thr	Ala	Ser	Asp	Asn	Leu	Ser	Glu	Ala	Arg	Ala	Met
			260					265					270		
Ile	Ala	Ala	Leu	Gln	Pro	Ala	Ala	Leu	Ser	Lys	Thr	Ser	Leu	Glu	Ala
		275					280					285			
Ala	Leu	His	Arg	Val	Thr	Glu	Pro	Leu	Leu	Gly	Ile	Asn	Phe	Val	Ile
	290					295					300				
Ser	Val	Asp	Gly	Asp	Val	Arg	Gln	Leu	Pro	Met	Lys	Thr	Glu	Ala	Thr
305					310					315					320
Leu	Leu	Arg	Ile	Ala	Gln	Gly	Ala	Ile	Gly	Asn	Val	Ala	Lys	His	Ser
			325					330						335	
Glu	Ala	Lys	Asn	Cys	His	Val	Thr	Leu	Thr	Tyr	Glu	Asp	Thr	Glu	Val
			340					345					350		
Arg	Leu	Asp	Val	Val	Asp	Asp	Gly	Val	Gly	Phe	Glu	Pro	Ser	Glu	Val
		355					360					365			
Ser	Ser	Thr	Pro	Ala	Gly	Leu	Gly	His	Ile	Gly	Leu	Thr	Ala	Leu	Gln
		370				375					380				
Gln	Arg	Ala	Met	Glu	Leu	His	Gly	Glu	Val	Ile	Val	Glu	Ser	Ala	Tyr
385					390					395					400
Gly	Gln	Gly	Thr	Ala	Val	Ser	Ala	Ala	Leu	Pro	Val	Glu	Pro	Pro	Glu
				405					410					415	
Gly	Phe	Val	Gly	Ala	Pro	Val	Leu	Ala	Asp	Ser	Asp	Ser	Ser	Ala	Thr
		420					425					430			
Gly	Glu	Val	Glu	Leu	Ser	Ser	Pro	Thr	Asp	Asp	Glu				
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<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXA00006

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 Met Val Asp Phe Asp
 1 5

acc atc gca gcc cga ctt gtc acc gaa aca gaa gaa gca atc atc tac 163
 Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu Glu Ala Ile Ile Tyr
 10 15 20.

gcc acc cgc gat gga ata atc aga ctc tgg aac ggc ggc tcc gag aaa 211
 Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn Gly Gly Ser Glu Lys
 25 30 35

ctc ttt gga tac acg gcc ggc gaa gcc ctt gga aaa tca ctc gac atc 259
 Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly Lys Ser Leu Asp Ile
 40 45 50

atc att ccc gaa aaa cac cgc aag gcc cac tgg gac gga tgg gat cgc 307
 Ile Ile Pro Glu Lys His Arg Lys Ala His Trp Asp Gly Trp Asp Arg
 55 60 65

gtc atg gaa tcc ggc gaa act cgc tat ggc tcc gaa ccg ctt aac gtt 355
 Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser Glu Pro Leu Asn Val
 70 75 80 85

cca ggc att cgt gcc gat gga tcc aaa atg tct ttg gaa ttc tcc atc 403
 Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser Leu Glu Phe Ser Ile
 90 95 100

acc atc ctg aag gac gat tcc gga aaa atc gaa ggc gtt gca gct ttt 451
 Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu Gly Val Ala Ala Phe
 105 110 115

ctc cgc gat gtc acc gcc aat tgg gat gag aaa aag gcc ctg cgg atc 499
 Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys Lys Ala Leu Arg Ile
 120 125 130

cga atc aaa gag ttg gaa cgc caa atc gag ggc cat taaggagatt 545
 Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly His
 135 140 145

cttgggtgcg cgg 558

<210> 36

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Val Asp Phe Asp Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu
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Glu Ala Ile Ile Tyr Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn
 20 25 30

Gly Gly Ser Glu Lys Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly
 35 40 45

Lys Ser Leu Asp Ile Ile Ile Pro Glu Lys His Arg Lys Ala His Trp
 50 55 60
 Asp Gly Trp Asp Arg Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser
 65 70 75 80
 Glu Pro Leu Asn Val Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser
 85 90 95
 Leu Glu Phe Ser Ile Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu
 100 105 110
 Gly Val Ala Ala Phe Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys
 115 120 125
 Lys Ala Leu Arg Ile Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly
 130 135 140
 His
 145

<210> 37
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(985)
 <223> RXA01860

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 Val Asn Pro Phe Ile 5
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 ctt gct gat cag ctg ctt tac gat gct aag cac gca ggt aga aat cgg 163
 Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His Ala Gly Arg Asn Arg 20
 10 15
 gtt gcg gtg cgc aga gct gaa aac acc att gtc cgc tca gct aag ccc 211
 Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val Arg Ser Ala Lys Pro 35
 25 30
 gca ttc tca gtt gag gaa ctt tcg gag atc ctg gag tca cat tct att 259
 Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu Glu Ser His Ser Ile 50
 40 45
 cgc ctc gag ctg cag ccg atc cta gaa ctt gaa aca ggt cgg gtg ggt 307
 Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu Thr Gly Arg Val Gly 65
 55 60
 gca gcc gaa ggt ctg ctc cga atc aac ttg gat ggc acc gat gtt cct 355
 Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp Gly Thr Asp Val Pro 85
 70 75 80
 acg ggg cag ttt gtt cag tcg gtt gaa cag gcc ggg cta gcc ccg aag 403
 Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala Gly Leu Ala Pro Lys

90	95	100	
ctt gat atc gca gtc atg aga gaa gga att aat cat att gag agg ctg Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn His Ile Glu Arg Leu 105 110 115			451
aga gct gtg tgt ccg act ttc agc ctc gct ttg aat ctg tcg ggc tat Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu Asn Leu Ser Gly Tyr 120 125 130			499
tct ctg agc tcg gcg aaa ata cgg gag gaa cta aga gcc gaa ttt aga Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu Arg Ala Glu Phe Arg 135 140 145			547
gct cgc gat ctg cca agg gga tca att agg ttt gag att act gag acc Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe Glu Ile Thr Glu Thr 150 155 160 165			595
gct ccg att gaa gac att gac gcg gca aaa gag ttt gtg cag atg ttg Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu Phe Val Gln Met Leu 170 175 180			643
aaa gat ttt ggc ttc cac atc gta atc gat gac ttt ggc gca gga cat Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp Phe Gly Ala Gly His 185 190 195			691
gag cct tat caa tat cta aag aag ttc gac ttt agc gtg ctg aag att Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe Ser Val Leu Lys Ile 200 205 210			739
gca ggt gaa ttc ata gaa ggt atg gtc acc aac cgc gtg gac cga agc Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn Arg Val Asp Arg Ser 215 220 225			787
atc gtc gaa tct att gct caa ctt gct aag gat gag gag atg gaa act Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp Glu Glu Met Glu Thr 230 235 240 245			835
gtc gcc gag ttt gtt tca agc aag gag att ttg gag gcg gta cga gag Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu Glu Ala Val Arg Glu 250 255 260			883
ata ggc gta acg tac gcc cag ggt ttc cat att ggt aaa tct aag ccg Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile Gly Lys Ser Lys Pro 265 270 275			931
att gat gaa ttt ata gct act tat ctc gag acg aac caa acc gct acc Ile Asp Glu Phe Ile Ala Thr Tyr Leu Glu Thr Asn Gln Thr Ala Thr 280 285 290			979
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<210> 38

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

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 Ala Gly Arg Asn Arg Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val
 20 25 30
 Arg Ser Ala Lys Pro Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu
 35 40 45
 Glu Ser His Ser Ile Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu
 50 55 60
 Thr Gly Arg Val Gly Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp
 65 70 75 80
 Gly Thr Asp Val Pro Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala
 85 90 95
 Gly Leu Ala Pro Lys Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn
 100 105 110
 His Ile Glu Arg Leu Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu
 115 120 125
 Asn Leu Ser Gly Tyr Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu
 130 135 140
 Arg Ala Glu Phe Arg Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe
 145 150 155 160
 Glu Ile Thr Glu Thr Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu
 165 170 175
 Phe Val Gln Met Leu Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp
 180 185 190
 Phe Gly Ala Gly His Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe
 195 200 205
 Ser Val Leu Lys Ile Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn
 210 215 220
 Arg Val Asp Arg Ser Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp
 225 230 235 240
 Glu Glu Met Glu Thr Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu
 245 250 255
 Glu Ala Val Arg Glu Ile Gly Val Thr Tyr Ala Gln Gly Phe His Ile
 260 265 270
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 275 280 285
 Asn Gln Thr Ala Thr Trp Gly
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<210> 39

<211> 2088

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2065)

<223> RXA01861

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cgtagtcgc aattgtgtgg ccatcagtgga gaatcgcgtgt	gtg	gtg	gcc	cgt	gac	115
	Val	Val	Ala	Arg	Asp	
	1			5		

ctg cag aag ctg gaa aaa ctt cgc ctg att tgt gga tac gtg ttt cta	163
Leu Gln Lys Leu Glu Lys Leu Arg Leu Ile Cys Gly Tyr Val Phe Leu	
10 15 20	

gtc cca gcc ata tac ctg cac ttt ttt gcg gaa acc tcc ctc agg gga	211
Val Pro Ala Ile Tyr Leu His Phe Phe Ala Glu Thr Ser Leu Arg Gly	
25 30 35	

gtg att ctg gca gga att gcg cac gct atc gca ggt cct ggc gtt gca	259
Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala Gly Pro Gly Val Ala	
40 45 50	

ctg gtt atg gca ttc atg gaa aat gcg caa ttg cca gaa ctg ttg cgt	307
Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu Pro Glu Leu Leu Arg	
55 60 65	

aaa cgg cat gca ttc gca ccc ttc tcc cat att cgc ctt cca ggc gat	355
Lys Arg His Ala Phe Ala Pro Phe Ser His Ile Arg Leu Pro Gly Asp	
70 75 80 85	

gta ttc cgg ctc ctc gtc gcg ggc att gtc atg gtc gca ata tcc aaa	403
Val Phe Arg Leu Leu Val Ala Gly Ile Val Met Val Ala Ile Ser Lys	
90 95 100	

ttg att gtg att ctt gct tat gca ctg gca gat ttg ccg tat tca ttc	451
Leu Ile Val Ile Leu Ala Tyr Ala Leu Ala Asp Leu Pro Tyr Ser Phe	
105 110 115	

acc ctt tat ctg acg atg gcc ctt cgt gac ttg act ggc att att gtg	499
Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu Thr Gly Ile Ile Val	
120 125 130	

gtt gcc ggg ccc gga att gca ctt tcg acg ccg ctg gta cta aat att	547
Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro Leu Val Leu Asn Ile	
135 140 145	

cac cga tca gca tgg cgc gag ttc gca gtt gtt atc ata gct acg gtc	595
His Arg Ser Ala Trp Arg Glu Phe Ala Val Val Ile Ile Ala Thr Val	
150 155 160 165	

gga gtg ctg gcg ctc att ttc gga ttt gct gtg gat ctt ccg acg gtc	643
Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val Asp Leu Pro Thr Val	
170 175 180	

tac ttg gca atg ttg cca ttg tat tgg agt gca acc cgt ctt cca gtg	691
Tyr Leu Ala Met Leu Pro Leu Tyr Trp Ser Ala Thr Arg Leu Pro Val	
185 190 195	

ctt tta gcc gtt ctt cat gcg gtg ttt act tca gca ata gtc gta att	739
Leu Leu Ala Val Leu His Ala Val Phe Thr Ser Ala Ile Val Val Ile	
200 205 210	
ctg tat ttc cta tta ggt acc gga tct ttt gcg att acg gat gaa tcc	787
Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala Ile Thr Asp Glu Ser	
215 220 225	
ata ctg gtg cag gca acg aca att cag ctt ttt gtt ctg atg tgt atc	835
Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe Val Leu Met Cys Ile	
230 235 240 245	
ttg ttg tcg cta gtt gtg tca acg aca gtc cag cag aca tca gca ctg	883
Leu Leu Ser Leu Val Val Ser Thr Thr Val Gln Gln Thr Ser Ala Leu	
250 255 260	
gtt gaa gag cta gag gtg gta gcg aag acc ctt cct gat gcg ctt ttt	931
Val Glu Glu Leu Glu Val Val Ala Lys Thr Leu Pro Asp Ala Leu Phe	
265 270 275	
atc gta aac aaa aat gga aca gca ttt cct gtt aac gca ggc gcg aaa	979
Ile Val Asn Lys Asn Gly Thr Ala Phe Pro Val Asn Ala Gly Ala Lys	
280 285 290	
aat ttc gtc aag caa tca ccg gat ggg cat tat tcc atg ccg aaa cta	1027
Asn Phe Val Lys Gln Ser Pro Asp Gly His Tyr Ser Met Pro Lys Leu	
295 300 305	
cag aat ata gac ggt gaa ccc atg gat gag aaa gaa agt ccg agc agt	1075
Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys Glu Ser Pro Ser Ser	
310 315 320 325	
atg gcc ttg cgt gga caa ggt gtc gaa gga gta tta gcc aag tta ggt	1123
Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val Leu Ala Lys Leu Gly	
330 335 340	
gaa gta ctg gga gaa gat ccg gac ttg gcg cgt cga atc ttc gaa att	1171
Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg Arg Ile Phe Glu Ile	
345 350 355	
agt gcc tca ccg atg tat ctg cgt gga gaa act gaa ccg ggt cat gcg	1219
Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr Glu Pro Gly His Ala	
360 365 370	
ctc gtg att tgg cat gac agt act aat gag tat tac acg atg caa caa	1267
Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr Tyr Thr Met Gln Gln	
375 380 385	
ttg acg ctt gca tat gaa gaa tcg cgg ctg cta ttt gaa aaa gcc cct	1315
Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu Phe Glu Lys Ala Pro	
390 395 400 405	
caa ggg att gcc atg ctg gac cct tcg gga gaa atc gta atg gcg aat	1363
Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu Ile Val Met Ala Asn	
410 415 420	
cga tcc ttt ggt gac ttg gtg gga acg act cct gtt cga ctc cta gga	1411
Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro Val Arg Leu Leu Gly	
425 430 435	

cga aat cta gag gat ttc gga gta gag gag gga acc atg gaa tac gtg	1459
Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly Thr Met Glu Tyr Val	
440 445 450	
acc cct gtt ctg tcg gac cca gaa gcc gtt gtg cac tta gat cgt tcg	1507
Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val His Leu Asp Arg Ser	
455 460 465	
ctc gaa aca ttg aga ggt aaa cag aaa aac gtt gct atg tca ttt agc	1555
Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val Ala Met Ser Phe Ser	
470 475 480 485	
tcg atg ggc aat gtt gga ggc aga atc gga act tta ctc gtt aat gtt	1603
Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr Leu Leu Val Asn Val	
490 495 500	
gtc gat gta acc gag cgc caa gaa ctc atc gag ctt gtg gag cat ttg	1651
Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu Leu Val Glu His Leu	
505 510 515	
gcg gat cat gac tcc ctg aca gga ttg gtc aat cgc agg cgg ctg gaa	1699
Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn Arg Arg Arg Leu Glu	
520 525 530	
tct gat atc gaa gag ctt atc ctc aag aat gaa cgc gat tcg acc gat	1747
Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu Arg Asp Ser Thr Asp	
535 540 545	
agt gca ttg ttg ctt ttg gat ctg gat tac ttc aag gaa gtt aat gat	1795
Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe Lys Glu Val Asn Asp	
550 555 560 565	
tcc ctc ggc cat gag gct ggt gac cag ttg ctt att gag ttt gct gag	1843
Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu Ile Glu Phe Ala Glu	
570 575 580	
atc ctc aaa gac agc gtg agg gat tcc gac att gtc gga cgc atc ggc	1891
Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile Val Gly Arg Ile Gly	
585 590 595	
ggc gat gaa ttc gtt att gtt ttg cct gac aca gac agg gat ggc gct	1939
Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr Asp Arg Asp Gly Ala	
600 605 610	
gaa gca atc ggt ata aga att att gag ttg gtc aat cag cac ttc aaa	1987
Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val Asn Gln His Phe Lys	
615 620 625	
ggc cga gga aaa gtg tta tcg cgg gtg tca agt aaa gta tcg gcg gga	2035
Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser Lys Val Ser Ala Gly	
630 635 640 645	
cgc tct ttt ctg atg ctc gtg ccc aag gtg tgaatccatt cattcttgct	2085
Arg Ser Phe Leu Met Leu Val Pro Lys Val	
650 655	
gat	2088

<210> 40

<211> 655

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 40

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			20					25						30	
Thr	Ser	Leu	Arg	Gly	Val	Ile	Leu	Ala	Gly	Ile	Ala	His	Ala	Ile	Ala
		35					40					45			
Gly	Pro	Gly	Val	Ala	Leu	Val	Met	Ala	Phe	Met	Glu	Asn	Ala	Gln	Leu
	50					55					60				
Pro	Glu	Leu	Leu	Arg	Lys	Arg	His	Ala	Phe	Ala	Pro	Phe	Ser	His	Ile
	65				70					75					80
Arg	Leu	Pro	Gly	Asp	Val	Phe	Arg	Leu	Leu	Val	Ala	Gly	Ile	Val	Met
				85					90					95	
Val	Ala	Ile	Ser	Lys	Leu	Ile	Val	Ile	Leu	Ala	Tyr	Ala	Leu	Ala	Asp
			100					105					110		
Leu	Pro	Tyr	Ser	Phe	Thr	Leu	Tyr	Leu	Thr	Met	Ala	Leu	Arg	Asp	Leu
		115					120					125			
Thr	Gly	Ile	Ile	Val	Val	Ala	Gly	Pro	Gly	Ile	Ala	Leu	Ser	Thr	Pro
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Leu	Val	Leu	Asn	Ile	His	Arg	Ser	Ala	Trp	Arg	Glu	Phe	Ala	Val	Val
145					150					155					160
Ile	Ile	Ala	Thr	Val	Gly	Val	Leu	Ala	Leu	Ile	Phe	Gly	Phe	Ala	Val
				165					170					175	
Asp	Leu	Pro	Thr	Val	Tyr	Leu	Ala	Met	Leu	Pro	Leu	Tyr	Trp	Ser	Ala
			180					185					190		
Thr	Arg	Leu	Pro	Val	Leu	Leu	Ala	Val	Leu	His	Ala	Val	Phe	Thr	Ser
		195					200					205			
Ala	Ile	Val	Val	Ile	Leu	Tyr	Phe	Leu	Leu	Gly	Thr	Gly	Ser	Phe	Ala
	210					215					220				
Ile	Thr	Asp	Glu	Ser	Ile	Leu	Val	Gln	Ala	Thr	Thr	Ile	Gln	Leu	Phe
225					230					235					240
Val	Leu	Met	Cys	Ile	Leu	Leu	Ser	Leu	Val	Val	Ser	Thr	Thr	Val	Gln
				245					250					255	
Gln	Thr	Ser	Ala	Leu	Val	Glu	Glu	Leu	Glu	Val	Val	Ala	Lys	Thr	Leu
			260					265					270		
Pro	Asp	Ala	Leu	Phe	Ile	Val	Asn	Lys	Asn	Gly	Thr	Ala	Phe	Pro	Val
		275					280					285			
Asn	Ala	Gly	Ala	Lys	Asn	Phe	Val	Lys	Gln	Ser	Pro	Asp	Gly	His	Tyr
	290					295					300				

Ser Met Pro Lys Leu Gln Asn Ile Asp Gly Glu Pro Met Asp Glu Lys
 305 310 315 320
 Glu Ser Pro Ser Ser Met Ala Leu Arg Gly Gln Gly Val Glu Gly Val
 325 330 335
 Leu Ala Lys Leu Gly Glu Val Leu Gly Glu Asp Pro Asp Leu Ala Arg
 340 345 350
 Arg Ile Phe Glu Ile Ser Ala Ser Pro Met Tyr Leu Arg Gly Glu Thr
 355 360 365
 Glu Pro Gly His Ala Leu Val Ile Trp His Asp Ser Thr Asn Glu Tyr
 370 375 380
 Tyr Thr Met Gln Gln Leu Thr Leu Ala Tyr Glu Glu Ser Arg Leu Leu
 385 390 395 400
 Phe Glu Lys Ala Pro Gln Gly Ile Ala Met Leu Asp Pro Ser Gly Glu
 405 410 415
 Ile Val Met Ala Asn Arg Ser Phe Gly Asp Leu Val Gly Thr Thr Pro
 420 425 430
 Val Arg Leu Leu Gly Arg Asn Leu Glu Asp Phe Gly Val Glu Glu Gly
 435 440 445
 Thr Met Glu Tyr Val Thr Pro Val Leu Ser Asp Pro Glu Ala Val Val
 450 455 460
 His Leu Asp Arg Ser Leu Glu Thr Leu Arg Gly Lys Gln Lys Asn Val
 465 470 475 480
 Ala Met Ser Phe Ser Ser Met Gly Asn Val Gly Gly Arg Ile Gly Thr
 485 490 495
 Leu Leu Val Asn Val Val Asp Val Thr Glu Arg Gln Glu Leu Ile Glu
 500 505 510
 Leu Val Glu His Leu Ala Asp His Asp Ser Leu Thr Gly Leu Val Asn
 515 520 525
 Arg Arg Arg Leu Glu Ser Asp Ile Glu Glu Leu Ile Leu Lys Asn Glu
 530 535 540
 Arg Asp Ser Thr Asp Ser Ala Leu Leu Leu Leu Asp Leu Asp Tyr Phe
 545 550 555 560
 Lys Glu Val Asn Asp Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu
 565 570 575
 Ile Glu Phe Ala Glu Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile
 580 585 590
 Val Gly Arg Ile Gly Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr
 595 600 605
 Asp Arg Asp Gly Ala Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val
 610 615 620
 Asn Gln His Phe Lys Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser

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Met Thr Ala Leu Ile																5
1																
cca gct cgc cac agc ctg act ttt cgt ctg ctc acc gcg cag ctt gct																163
Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu Thr Ala Gln Leu Ala																20
10 15																
gtg gtg ttg atc agt ctg ctg gcc gcc ctg att gtg gct gcc ttg gta																211
Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile Val Ala Ala Leu Val																35
25 30																
ggg cct gca att ttc aat tct cac ctg gat ctt tcc ggc ccg att gat																259
Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu Ser Gly Pro Ile Asp																50
40 45																
ccc cgc cag acg gat ttc cac att cag gag gcc tac cgg gac gcc aat																307
Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala Tyr Arg Asp Ala Asn																65
55 60																
tac att gcc ctc gca gcg gca ctt ccc acc gca gtg ttg agc tcc att																355
Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala Val Leu Ser Ser Ile																85
70 75 80																
ggt gtg agt ttt tgg ctt tcc cac cgc ctg ggc cag ccg ttg tgg cga																403
Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly Gln Pro Leu Trp Arg																100
90 95																
ctg tcc cgg gct gca act gcc atg agc tcc ggc gac tac cag gtg cgc																451
Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly Asp Tyr Gln Val Arg																115
105 110																
gta ccc att tcc gat gtg gat aaa gag gtc gct gct cta tct ctc gcc																499
Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala Ala Leu Ser Leu Ala																120 125 130
135 140 145																
ttc aat tcc atg gcg gat cag ctc gaa cac aca gaa gaa ctc cgc cga																547
Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr Glu Glu Leu Arg Arg																135 140 145
135 140 145																
aac atg ctc tcc gat cta tcc cat gaa atg aac act ccc ctt tcc gtc																595
Asn Met Leu Ser Asp Leu Ser His Glu Met Asn Thr Pro Leu Ser Val																120 125 130

150	155	160	165	
ctc ctt gtt tat gtc gac ggt ttg cag gac ggc atg gtg gag tgg gac				643
Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly Met Val Glu Trp Asp	170	175	180	
gcc gac acc cac gca gtt ttc gcc gag caa ctt ggc cgg ctt tcc cgc				691
Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu Gly Arg Leu Ser Arg	185	190	195	
ctc aca tca gat ctt gat gat gtc tct aga gcc caa gaa cac cgc ttc				739
Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala Gln Glu His Arg Phe	200	205	210	
gac ctg gtc tac agc acc gtc gcc atc ggt ggt ctc att cac aat gcc				787
Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly Leu Ile His Asn Ala	215	220	225	
gcc gga gcc gcc gca ggt tcc tac caa gaa aaa ggc gtg gcc ctg gaa				835
Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys Gly Val Ala Leu Glu	230	235	240	245
gta aca ggc agc gat tcc acc gaa ctc atc cgc gtt gat agc caa cgc				883
Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg Val Asp Ser Gln Arg	250	255	260	
ttc gcc caa gtc atg gcc aac ctc ttc tcc aac gcc ttg cgg cac acc				931
Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn Ala Leu Arg His Thr	265	270	275	
ccc gcc ggt ggg aaa gtt cac gtc cgc gtc ctg cgt caa ggc gtg gga				979
Pro Ala Gly Lys Val His Val Arg Val Leu Arg Gln Gly Val Gly	280	285	290	
acc atc gtc atc gaa gtc ata gac aac ggc gaa gga atc gcc cct gaa				1027
Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu Gly Ile Ala Pro Glu	295	300	305	
cac gta aaa tac gtt ttc gaa cgc tac ttc cgc gcc aaa cga tcc gac				1075
His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg Ala Lys Arg Ser Asp	310	315	320	325
tcc gac gac caa tcc ggc tcc gga atc ggc ctc acc atc tcc cgc gca				1123
Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu Thr Ile Ser Arg Ala	330	335	340	
ctc atc gaa gcg caa ggt ggc aca cta acc gca gaa tcc gct ggc ctg				1171
Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala Glu Ser Ala Gly Leu	345	350	355	
ggc aaa ggc gcg aaa ttt acc atc cga cta ccc ctt tta agc aaa				1216
Gly Lys Gly Ala Lys Phe Thr Ile Arg Leu Pro Leu Leu Ser Lys	360	365	370	
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<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Met Thr Ala Leu Ile Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu
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Thr Ala Gln Leu Ala Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile
          20           25           30

Val Ala Ala Leu Val Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu
          35           40           45

Ser Gly Pro Ile Asp Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala
 50           55           60

Tyr Arg Asp Ala Asn Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala
 65           70           75           80

Val Leu Ser Ser Ile Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly
          85           90           95

Gln Pro Leu Trp Arg Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly
          100           105           110

Asp Tyr Gln Val Arg Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala
 115           120           125

Ala Leu Ser Leu Ala Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr
 130           135           140

Glu Glu Leu Arg Arg Asn Met Leu Ser Asp Leu Ser His Glu Met Asn
 145           150           155           160

Thr Pro Leu Ser Val Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly
          165           170           175

Met Val Glu Trp Asp Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu
          180           185           190

Gly Arg Leu Ser Arg Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala
          195           200           205

Gln Glu His Arg Phe Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly
 210           215           220

Leu Ile His Asn Ala Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys
 225           230           235           240

Gly Val Ala Leu Glu Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg
          245           250           255

Val Asp Ser Gln Arg Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn
          260           265           270

Ala Leu Arg His Thr Pro Ala Gly Gly Lys Val His Val Arg Val Leu
          275           280           285

Arg Gln Gly Val Gly Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu
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Gly Ile Ala Pro Glu His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg
 305           310           315           320

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<400> 43																
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ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc																115
Met Asn Lys Asp Phe																5
tgg acc gca ggc tgg acc gcc cgc tgg ttt tgc cgc ggg gtt tcc ctt																163
Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser Arg Gly Val Ser Leu																10 15 20
ttg gcc agc cca gtt acc gcc cca ctg aac tct tgg cgg aga ttg cct																211
Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro																25 30 35
aac ttg gcc aag tac acc ctc tac acc agg gtg tgc ttg caa gcg atc																259
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile																40 45 50
ccc gtg gtg ttg ctg tgc gcg tat ttc ctg ggc atc gta gct aat gca																307
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala																55 60 65
ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tgc gtc atc																355
Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu Gly Phe Ser Val Ile																70 75 80 85
ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tgc ctg aat																403
Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn																90 95 100
tct cat cct agg cgc agc gta cag ccg ttc ttc ttc acc ggg ttg gtg																451
Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val																105 110 115
ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att ccg ggc																499
Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly																

120	125	130	
tta aac atg tcg gac aac acc cga gca act gcc ctt att ttc act ctt Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu 135 140 145			547
acc tgc gta ttt ctg ctt tcg atc gcc tac att ccg tgg atg aat tac Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr 150 155 160 165			595
cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Thr Ser 170 175 180			643
aca acg act gat tat tta agt gca ttg tgg gtg gtt atc ccg cca ctc Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu 185 190 195			691
atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys 200 205 210			739
gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu 215 220 225			787
gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His 230 235 240 245			835
ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Lys 250 255 260			883
cgc ggc gac gac cgc ctc gaa aac gag ctg cgt gag ctc caa aaa ctc Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg Glu Leu Gln Lys Leu 265 270 275			931
acc cgc acc tcc atg tcg gaa atg cgc gac gtc gtc tcc ggc tac cgc Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val Val Ser Gly Tyr Arg 280 285 290			979
acc gtc aac ctc gcc acg gaa atc gag ggc gct aaa agt ttg ctt gcc Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala Lys Ser Leu Leu Ala 295 300 305			1027
gac gcc cac atc cac ctt tcc gtc atc ggc acc acg tcc cag gtg tca Asp Ala His Ile His Leu Ser Val Ile Gly Thr Thr Ser Gln Val Ser 310 315 320 325			1075
ccc gct cac cga gaa ctg tgc gcg tgg ctt gtc cgg gaa gcc acc aca Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val Arg Glu Ala Thr Thr 330 335 340			1123
aac att ctg cgc cac tct gat gca acg gat gcc acc ctc acg ttg agc Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala Thr Leu Thr Leu Ser 345 350 355			1171
agc aca gag gtg cgc atg gac aac aat ggt gtg aac aag gac atc ggc Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val Asn Lys Asp Ile Gly 360 365 370			1219

aga ctc tct ggt ctc agc gcc ctg cgc tca cga gcg gaa tca gcc gga 1267
 Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg Ala Glu Ser Ala Gly
 375 380 385

atg acg ctc att gtg tcc cgc gaa gac gac cag ttc agc gtc cgc atg 1315
 Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln Phe Ser Val Arg Met
 390 395 400 405

ctc att aat gca cct gca aat aca cct gca gaa aag gaa gct 1357
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 410 415

taaatgattt ccatttccat cgc 1380

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<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

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 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
 130 135 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
 145 150 155 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
 165 170 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
 180 185 190

Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
 195 200 205

Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
 210 215 220
 Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
 225 230 235 240
 Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
 245 250 255
 Leu Ala Leu Ala Lys Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg
 260 265 270
 Glu Leu Gln Lys Leu Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val
 275 280 285
 Val Ser Gly Tyr Arg Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala
 290 295 300
 Lys Ser Leu Leu Ala Asp Ala His Ile His Leu Ser Val Ile Gly Thr
 305 310 315 320
 Thr Ser Gln Val Ser Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val
 325 330 335
 Arg Glu Ala Thr Thr Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala
 340 345 350
 Thr Leu Thr Leu Ser Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val
 355 360 365
 Asn Lys Asp Ile Gly Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg
 370 375 380
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 385 390 395 400
 Phe Ser Val Arg Met Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu
 405 410 415
 Lys Glu Ala

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 <212> DNA
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<220>
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 <223> FRXA01211

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 Met Asn Lys Asp Phe
 1 5

tgg acc gca ggc tgg acc gcc cgc tgg ttt tcg cgc ggg gtt tcc ctt 163

Trp	Thr	Ala	Gly	Trp	Thr	Ala	Arg	Trp	Phe	Ser	Arg	Gly	Val	Ser	Leu	
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ttg	gcc	agc	cca	gtt	acc	gcc	cca	ctg	aac	tct	tgg	cgg	aga	ttg	cct	211
Leu	Ala	Ser	Pro	Val	Thr	Ala	Pro	Leu	Asn	Ser	Trp	Arg	Arg	Leu	Pro	
			25					30					35			
aac	ttg	gcc	aag	tac	acc	ctc	tac	acc	agg	gtg	tcg	ttg	caa	gcg	atc	259
Asn	Leu	Ala	Lys	Tyr	Thr	Leu	Tyr	Thr	Arg	Val	Ser	Leu	Gln	Ala	Ile	
		40					45					50				
ccc	gtg	gtg	ttg	ctg	tcg	gcg	tat	ttc	ctg	ggc	atc	gta	gct	aat	gca	307
Pro	Val	Val	Leu	Leu	Ser	Ala	Tyr	Phe	Leu	Gly	Ile	Val	Ala	Asn	Ala	
	55					60					65					
ggc	acc	ctg	aat	ccc	tca	ttt	gtg	tgg	ctg	ctg	ggt	ttc	tcg	gtc	atc	355
Gly	Thr	Leu	Asn	Pro	Ser	Phe	Val	Trp	Leu	Leu	Gly	Phe	Ser	Val	Ile	
70					75				80						85	
ctt	tta	ata	gtg	acg	gta	ttg	gtt	tat	gaa	tat	cag	cca	tcg	ctg	aat	403
Leu	Leu	Ile	Val	Thr	Val	Leu	Val	Tyr	Glu	Tyr	Gln	Pro	Ser	Leu	Asn	
				90					95					100		
tct	cat	cct	agg	cgc	agc	gta	cag	ccg	ttc	ttc	ttc	acc	ggg	ttg	gtg	451
Ser	His	Pro	Arg	Arg	Ser	Val	Gln	Pro	Phe	Phe	Phe	Thr	Gly	Leu	Val	
			105					110					115			
ctc	aac	gtt	tta	ggc	gtt	gtg	gtg	tct	gtg	gtg	ctt	caa	att	ccg	ggc	499
Leu	Asn	Val	Leu	Gly	Val	Val	Val	Ser	Val	Val	Leu	Gln	Ile	Pro	Gly	
		120					125					130				
tta	aac	atg	tcg	gac	aac	acc	cga	gca	act	gcc	ctt	att	ttc	act	ctt	547
Leu	Asn	Met	Ser	Asp	Asn	Thr	Arg	Ala	Thr	Ala	Leu	Ile	Phe	Thr	Leu	
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Thr	Cys	Val	Phe	Leu	Leu	Ser	Ile	Ala	Tyr	Ile	Pro	Trp	Met	Asn	Tyr	
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cga	tgg	gtt	tgg	ctg	atc	gca	atg	tct	gca	gtg	ttg	tgg	tgg	acc	agc	643
Arg	Trp	Val	Trp	Leu	Ile	Ala	Met	Ser	Ala	Val	Leu	Trp	Trp	Thr	Ser	
				170					175					180		
aca	acg	act	gat	tat	tta	agt	gca	ttg	tgg	gtg	gtt	atc	ccg	cca	ctc	691
Thr	Thr	Thr	Asp	Tyr	Leu	Ser	Ala	Leu	Trp	Val	Val	Ile	Pro	Pro	Leu	
			185					190					195			
atg	gca	gga	acc	gtc	cga	ctt	tcc	gta	tgg	acc	gtc	gat	gtc	atg	aaa	739
Met	Ala	Gly	Thr	Val	Arg	Leu	Ser	Val	Trp	Thr	Val	Asp	Val	Met	Lys	
		200					205					210				
gag	gtt	gag	cgt	tcc	cgc	gaa	ttg	gaa	gcc	tcc	ctc	cgc	gtc	acc	gaa	787
Glu	Val	Glu	Arg	Ser	Arg	Glu	Leu	Glu	Ala	Ser	Leu	Arg	Val	Thr	Glu	
	215					220					225					
gaa	cgc	ctt	cgt	ttc	gcc	cag	gaa	ctc	cac	gac	act	tta	gga	caa	cac	835
Glu	Arg	Leu	Arg	Phe	Ala	Gln	Glu	Leu	His	Asp	Thr	Leu	Gly	Gln	His	
230					235					240					245	
ctg	gcg	gca	atg	tcc	gtg	aaa	tca	gaa	ctg	gcg	ctt	gcc	ctg	gcg	aaa	883
Leu	Ala	Ala	Met	Ser	Val	Lys	Ser	Glu	Leu	Ala	Leu	Ala	Leu	Ala	Lys	

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 Arg Gly Asp Asp
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 <210> 46
 <211> 265
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
 50 55 60
 Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65 70 75 80
 Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
 85 90 95
 Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
 100 105 110
 Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
 115 120 125
 Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
 130 135 140
 Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
 145 150 155 160
 Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
 165 170 175
 Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
 180 185 190
 Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
 195 200 205
 Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
 210 215 220
 Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
 225 230 235 240
 Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
 245 250 255

Leu Ala Leu Ala Lys Arg Gly Asp Asp
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<210> 47
 <211> 529
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(529)
 <223> RXA01248

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 Met Ala Asp Arg Thr
 1 5
 ccg acc acc gcc acg ccc ccg ggg cgg gtg ctg gtc gtc gat gat gaa 163
 Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu Val Val Asp Asp Glu
 10 15 20
 caa ccc ctg gct cag atg gtg gcc tcc tac ctc atc cgg gcc ggc ttc 211
 Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu Ile Arg Ala Gly Phe
 25 30 35
 gac acc cgc cag gcg cac acc ggc acc cag gcc gtg gac gag gcc cgt 259
 Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala Val Asp Glu Ala Arg
 40 45 50
 cgc ttt tcc ccc gat gtt gtg gtg ctg gat ctg ggg ctg ccc gaa ctc 307
 Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu Gly Leu Pro Glu Leu
 55 60 65
 gac ggc ctg gag gtg tgc cga cgg atc cgc acc ttc tcg gac tgc tac 355
 Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr Phe Ser Asp Cys Tyr
 70 75 80 85
 atc ctc atg ctc acc gcg cgt ggc agc gag gac gac aag atc agc ggt 403
 Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp Asp Lys Ile Ser Gly
 90 95 100
 ttg acc ctg ggg gcg gat gac tac atc acc aaa cct ttt agc atc cgg 451
 Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Ser Ile Arg
 105 110 115
 gaa ctg gtg acc cgg gtg cat gcg gtg ctg cgc cgc ccg cgc acc agc 499
 Glu Leu Val Thr Arg Val His Ala Val Leu Arg Arg Pro Arg Thr Ser
 120 125 130
 acc acc cca ccg cag gtg acc acc ccc ttg 529
 Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
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<210> 48
 <211> 143
 <212> PRT

<213> Corynebacterium glutamicum

<400> 48

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 Ile Arg Ala Gly Phe Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala
 35 40 45
 Val Asp Glu Ala Arg Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu
 50 55 60
 Gly Leu Pro Glu Leu Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr
 65 70 75 80
 Phe Ser Asp Cys Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp
 85 90 95
 Asp Lys Ile Ser Gly Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys
 100 105 110
 Pro Phe Ser Ile Arg Glu Leu Val Thr Arg Val His Ala Val Leu Arg
 115 120 125
 Arg Pro Arg Thr Ser Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
 130 135 140

<210> 49

<211> 846

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(823)

<223> RXA02668

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 Met Thr Asn Pro Ser
 1 5
 ccc gcg cta aat gaa acc ctt tcc ggc agg gtg ctg atc gtt gaa gat 163
 Pro Ala Leu Asn Glu Thr Leu Ser Gly Arg Val Leu Ile Val Glu Asp
 10 15 20
 gag cgc cct ctt gct cgc atg att tcg ctt tat tta agc aaa gcg ggt 211
 Glu Arg Pro Leu Ala Arg Met Ile Ser Leu Tyr Leu Ser Lys Ala Gly
 25 30 35
 ttc gat acc acc acg atc cac gac ggc gcc gct gct cca gat aag gtc 259
 Phe Asp Thr Thr Thr Ile His Asp Gly Ala Ala Ala Pro Asp Lys Val
 40 45 50
 gct cac ctg cgc ccc gac gtg gtc att ttg gat ctt ggg ctg cct ggt 307

Ala His Leu Arg Pro Asp Val Val Ile Leu Asp Leu Gly Leu Pro Gly
55 60 65

ctt gat ggt ttg gaa gtg tgc aaa cgc atc cgc gcg ttc acc gat tgc 355
Leu Asp Gly Leu Glu Val Cys Lys Arg Ile Arg Ala Phe Thr Asp Cys
70 75 80 85

tac atc cta atg ctc acc gcc agg ggt tca gag cgg gat cgg att aca 403
Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Arg Asp Arg Ile Thr
90 95 100

ggg ttg gaa att ggg gct gat gat tac atc acc aag ccg ttt aat atc 451
Gly Leu Glu Ile Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Asn Ile
105 110 115

cgc gaa ctt gtc att cgt atc cag tca gta atg cgt cgc cct cga aaa 499
Arg Glu Leu Val Ile Arg Ile Gln Ser Val Met Arg Arg Pro Arg Lys
120 125 130

atc gat gaa acc atc caa aat ggt ttg acc ttg act tat ggc cac att 547
Ile Asp Glu Thr Ile Gln Asn Gly Leu Thr Leu Thr Tyr Gly His Ile
135 140 145

gag ctg gac acc ttg gcg cat gaa gtc act gtc aaa ggc gtt ggg gtg 595
Glu Leu Asp Thr Leu Ala His Glu Val Thr Val Lys Gly Val Gly Val
150 155 160 165

aca ctg acc cgc aca gaa ttt gag ctg ctt caa gcc ctc atg cac aaa 643
Thr Leu Thr Arg Thr Glu Phe Glu Leu Leu Gln Ala Leu Met His Lys
170 175 180

ccg gga gag gca gtg tct agg cgt gat ttg gtc agc caa gtg tgg gat 691
Pro Gly Glu Ala Val Ser Arg Arg Asp Leu Val Ser Gln Val Trp Asp
185 190 195

acc acc tgg gtt ggc gat gaa cgc atc gtt gac gtg cac att gga aat 739
Thr Thr Trp Val Gly Asp Glu Arg Ile Val Asp Val His Ile Gly Asn
200 205 210

ctg cgc cgc aag ctg gaa gca cct gcg ccg ggt tca cac ttc atc gac 787
Leu Arg Arg Lys Leu Glu Ala Pro Ala Pro Gly Ser His Phe Ile Asp
215 220 225

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catcccagct cgc 846

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<213> Corynebacterium glutamicum

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20 25 30

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35 40 45

Ala Pro Asp Lys Val Ala His Leu Arg Pro Asp Val Val Ile Leu Asp
50 55 60

Leu Gly Leu Pro Gly Leu Asp Gly Leu Glu Val Cys Lys Arg Ile Arg
65 70 75 80

Ala Phe Thr Asp Cys Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu
85 90 95

Arg Asp Arg Ile Thr Gly Leu Glu Ile Gly Ala Asp Asp Tyr Ile Thr
100 105 110

Lys Pro Phe Asn Ile Arg Glu Leu Val Ile Arg Ile Gln Ser Val Met
115 120 125

Arg Arg Pro Arg Lys Ile Asp Glu Thr Ile Gln Asn Gly Leu Thr Leu
130 135 140

Thr Tyr Gly His Ile Glu Leu Asp Thr Leu Ala His Glu Val Thr Val
145 150 155 160

Lys Gly Val Gly Val Thr Leu Thr Arg Thr Glu Phe Glu Leu Leu Gln
165 170 175

Ala Leu Met His Lys Pro Gly Glu Ala Val Ser Arg Arg Asp Leu Val
180 185 190

Ser Gln Val Trp Asp Thr Thr Trp Val Gly Asp Glu Arg Ile Val Asp
195 200 205

Val His Ile Gly Asn Leu Arg Arg Lys Leu Glu Ala Pro Ala Pro Gly
210 215 220

Ser His Phe Ile Asp Thr Ile Arg Gly Val Gly Tyr Arg Met Ala Phe
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Lys

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<211> 819

<212> DNA

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Met Lys Ile Leu Val

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5

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Phe Asn Gly Tyr Asn Val Val Leu Ala Glu Asp Gly Ile Gln Ala Leu	
25 30 35	
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Glu Met Ile Asp Lys Glu Gln Pro Ala Leu Val Ile Leu Asp Val Met	
40 45 50	
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Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg His Leu Arg Ser Glu	
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ggc gat gat cgg cca att ctt att ctt act gcc cgc gat aat gtt tct	355
Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala Arg Asp Asn Val Ser	
70 75 80 85	
gat cgt gtt ggt ggc ctc gat gca ggc gca gat gac tat ttg gct aaa	403
Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp Asp Tyr Leu Ala Lys	
90 95 100	
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Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val Arg Ser Leu Val Arg	
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120 125 130	
tta tct tgt ggc gat ttg acg ctt gac cca gaa agt cga gat gtc tac	547
Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu Ser Arg Asp Val Tyr	
135 140 145	
cgc aac gga cgc gcc atc agc ctt act cga aca gag ttc gcg ctc ctg	595
Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr Glu Phe Ala Leu Leu	
150 155 160 165	
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Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu Thr Arg Ala Gln Ile	
170 175 180	
ttg gaa gag gta tgg ggc tgc gat ttc ccc act tca ggc aat gcc ctc	691
Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr Ser Gly Asn Ala Leu	
185 190 195	
gag gtc tac att gga tac ctt cga cgc aag act gaa ttg gaa gga gaa	739
Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr Glu Leu Glu Gly Glu	
200 205 210	
gac cgc ctg atc cat aca gta cga gga gtc gga tac gtc ctg cga gag	787
Asp Arg Leu Ile His Thr Val Arg Gly Val Gly Tyr Val Leu Arg Glu	
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Thr Ala Pro	
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ile Leu Asp Val Met Met Pro Gly Met Asp Gly Leu Glu Val Cys Arg
 50 55 60
 His Leu Arg Ser Glu Gly Asp Asp Arg Pro Ile Leu Ile Leu Thr Ala
 65 70 75 80
 Arg Asp Asn Val Ser Asp Arg Val Gly Gly Leu Asp Ala Gly Ala Asp
 85 90 95
 Asp Tyr Leu Ala Lys Pro Phe Ala Leu Glu Glu Leu Leu Ala Arg Val
 100 105 110
 Arg Ser Leu Val Arg Arg Ser Ala Val Glu Ser Asn Gln Ser Ser Ser
 115 120 125
 Ile Glu Gln Ala Leu Leu Ser Cys Gly Asp Leu Thr Leu Asp Pro Glu
 130 135 140
 Ser Arg Asp Val Tyr Arg Asn Gly Arg Ala Ile Ser Leu Thr Arg Thr
 145 150 155 160
 Glu Phe Ala Leu Leu Gln Leu Leu Leu Lys Asn Gln Arg Lys Val Leu
 165 170 175
 Thr Arg Ala Gln Ile Leu Glu Glu Val Trp Gly Cys Asp Phe Pro Thr
 180 185 190
 Ser Gly Asn Ala Leu Glu Val Tyr Ile Gly Tyr Leu Arg Arg Lys Thr
 195 200 205
 Glu Leu Glu Gly Glu Asp Arg Leu Ile His Thr Val Arg Gly Val Gly
 210 215 220
 Tyr Val Leu Arg Glu Thr Ala Pro
 225 230

<210> 53
 <211> 1488
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1465)
 <223> RXA02631

<400> 53

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Arg Leu Ala Leu Leu Ser Ala Thr Leu Val Ala Phe Ala Val Gly Val
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att act gtt gct gca tat tgg tct gtc tcc agc tat gtc acc aac tca 211
Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser Tyr Val Thr Asn Ser
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atc gat cgt gat ctg gaa aaa caa gcg gat gca atg ctt gga cga gcc 259
Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala Met Leu Gly Arg Ala
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Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr Glu Ile Ala Leu Leu
                        55                        60                        65

ggt gaa tat gcc agt gac act cga atc gcc tta atc cca cct ggg tgg 355
Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu Ile Pro Pro Gly Trp
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gaa tac gtc atc ggt gaa tcc ata tca ctg cct gat tca gat ttc ctt 403
Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro Asp Ser Asp Phe Leu
                        90                        95                        100

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Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val Thr Ser Ala Glu Arg
                        105                        110                        115

att ctc atg aaa cga gat agc tcg ggc aca gtg gtg gtt ttt gct aaa 499
Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val Val Val Phe Ala Lys
                        120                        125                        130

gat atg gtg gat acc gat cgg cag ctc acg gtg ctt ggc gtc att ctc 547
Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val Leu Gly Val Ile Leu
                        135                        140                        145

ttg atc att ggc ggc agt ggt gtt ttg gcg tcg att ctg ctt ggt ttc 595
Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser Ile Leu Leu Gly Phe
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atc att gcg aag gag ggg ctg aaa cca ctg tca aag ctg cag cgt gcc 643
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                        170                        175                        180

gtc gaa gag atc gaa cga act gat gag ctt cgt gcg att ccc gtg gtg 691
Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg Ala Ile Pro Val Val
                        185                        190                        195

gga aat gat gag ttc gct aag ttg act cgt agt ttc aat gac atg ctc 739
Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser Phe Asn Asp Met Leu
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<213> *Corynebacterium glutamicum*

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 20 25 30

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 35 40 45

Met Leu Gly Arg Ala Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr
 50 55 60

Glu Ile Ala Leu Leu Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu
 65 70 75 80

Ile Pro Pro Gly Trp Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro
 85 90 95

Asp Ser Asp Phe Leu Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val
 100 105 110

Thr Ser Ala Glu Arg Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val
 115 120 125

Val Val Phe Ala Lys Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val
 130 135 140

Leu Gly Val Ile Leu Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser
 145 150 155 160

Ile Leu Leu Gly Phe Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser
 165 170 175

Lys Leu Gln Arg Ala Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg
 180 185 190

Ala Ile Pro Val Val Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser
 195 200 205

Phe Asn Asp Met Leu Lys Ala Leu Arg Glu Ser Arg Thr Arg Gln Ser
 210 215 220

Gln Leu Val Ala Asp Ala Gly His Glu Leu Lys Thr Pro Leu Thr Ser
 225 230 235 240

Met Arg Thr Asn Ile Glu Leu Leu Leu Met Ala Thr Asn Ser Gly Gly
 245 250 255

Ser Gly Ile Pro Lys Glu Glu Leu Asp Gly Leu Gln Arg Asp Val Leu
 260 265 270

Ala Gln Met Thr Glu Met Ser Asp Leu Ile Gly Asp Leu Val Asp Leu

275					280					285					
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305					310					315					
Arg	Ile	Asp	Val	Ser	Glu	Thr	Val	Asp	Trp	Lys	Leu	Leu	Gly	Asp	Asp
325					330					335					
Phe	Ser	Leu	Thr	Arg	Ala	Leu	Val	Asn	Val	Leu	Asp	Asn	Ala	Ile	Lys
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Trp	Ser	Pro	Glu	Asn	Gly	Ile	Val	Arg	Val	Ser	Met	Ser	Gln	Ile	Asp
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Glu	Lys	Glu	Arg	Gly	Leu	Val	Leu	Glu	Arg	Phe	Tyr	Arg	Ala	Val	Ser
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420					425					430					
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 Met Ser Lys Ile Leu
 1 5
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 Leu Ala Glu Asp Asp Ala Gly Ile Ala Asp Phe Ile Val Arg Gly Leu
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 atc cgc gaa ggc ttc gaa tgc gag gtc acc gaa tcc ggc gcc gaa gct 211
 Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu Ser Gly Ala Glu Ala
 25 30 35

ttc gcc cgc gca cat tcc ggc gat ttc gat ctc atg gtt tta gac ctc 259
 Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu Met Val Leu Asp Leu
 40 45 50

ggc ctc ccc cac atg gac ggc acg gat gtc cta gag caa tta aga aat 307
 Gly Leu Pro His Met Asp Gly Thr Asp Val Leu Glu Gln Leu Arg Asn
 55 60 65

ctg cag gtc acg cta cct atc att gtg ctc acg gca cgc acc aac atc 355
 Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr Ala Arg Thr Asn Ile
 70 75 80 85

gag gac cgc ctc cgc acc ctc gag ggc ggc gcc gac gat tac atg ccc 403
 Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala Asp Asp Tyr Met Pro
 90 95 100

aaa cca ttc caa ttc gca gaa tta ctg gcc cgc atc aaa ctc cgc ctc 451
 Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg Ile Lys Leu Arg Leu
 105 110 115

gcc aaa cac act cct cag gaa acg ccg acc gat gcg cgc gtg cta cga 499
 Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp Ala Arg Val Leu Arg
 120 125 130

aac ggc gat ttg gag ctc gat ctt cgt acc cag cgt gtg ctc atc gac 547
 Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln Arg Val Leu Ile Asp
 135 140 145

ggc tcc tgg cac gac ctt tcc cgc cgc gaa gtc gat ctg ctc gaa acc 595
 Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val Asp Leu Leu Glu Thr
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ctc atg cga cac cca ggg caa atc ctc tcc cga gtc caa ctc ctc cga 643
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 170 175 180

ctg gtg tgg gac atg gat tgg gac ccc ggc tca aac gtg gtg gac gta 691
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 185 190 195

tat atc cgc gcg ttg agg aag aaa atc ggt gcc cat cgg gtc gaa acc 739
 Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala His Arg Val Glu Thr
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atc cga gga tct ggc tac cgg ctg cgc taactgcaga acgagaccaa aaa 789
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<210> 56

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Met Val Leu Asp Leu Gly Leu Pro His Met Asp Gly Thr Asp Val Leu
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Glu Gln Leu Arg Asn Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr
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Ala Arg Thr Asn Ile Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala
85 90 95

Asp Asp Tyr Met Pro Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg
100 105 110

Ile Lys Leu Arg Leu Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp
115 120 125

Ala Arg Val Leu Arg Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln
130 135 140

Arg Val Leu Ile Asp Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val
145 150 155 160

Asp Leu Leu Glu Thr Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg
165 170 175

Val Gln Leu Leu Arg Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser
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Asn Val Val Asp Val Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala
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<223> RXA00284

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Met Ala Arg Lys Leu
1 5

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Lys Asp Lys Leu Pro Arg Ser Phe Asp Lys Ile Val Glu Ser Gly Asp
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Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg Ala Leu Asp Ala Lys
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Asn Arg His Gly Asn Thr Ala Leu His Met Arg Gly Val Pro Glu Glu	
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Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp Val Asp Ile Arg Asn	
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Glu Asp Gly Asp Thr Pro Leu His Val His Ser His Asp Trp Asn Leu	
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Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp Val Cys Ala Val Asn	
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aat gaa ggc gaa tcg gtt gcc tac tcc gct gcc ttc ttc cca gaa aac	451
Asn Glu Gly Glu Ser Val Ala Tyr Ser Ala Ala Phe Phe Pro Glu Asn	
105 110 115	
ctc aaa aag ctt atc gac gcc ggc gcc gac ccc tac tcg cgc gcc aac	499
Leu Lys Lys Leu Ile Asp Ala Gly Ala Asp Pro Tyr Ser Arg Ala Asn	
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Asp Gly Thr Thr Pro Leu Met Arg Val Ile Arg Ser Ala Asp Thr Gly	
135 140 145	
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Gln Ile Ile Glu Leu Ala Glu Ile Thr Lys Leu Leu Ser Gly Thr Glu	
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170 175 180	
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Gly Glu Arg Phe Glu Asp Val Arg Glu Val Tyr Asn Glu Glu Ser Val	
185 190 195	
gac caa gca tct gcg gac atg atc tgg ctc tac gat cgt ttc gac atc	739
Asp Gln Ala Ser Ala Asp Met Ile Trp Leu Tyr Asp Arg Phe Asp Ile	
200 205 210	
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Pro Glu Glu Leu Arg Ala Asn Thr Pro Ile Leu His Asp Gly Val Ser	
215 220 225	
cca ata gaa ctg cct ggg gat acc tgg caa gaa caa ttc atc gaa ggc	835
Pro Ile Glu Leu Pro Gly Asp Thr Trp Gln Glu Gln Phe Ile Glu Gly	
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Tyr Asp Leu Leu Val Pro Ala Met Gly Lys Ala Lys Ser Leu Gln Gly	
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Glu Ala Ile Arg Ile Ala Gly Arg Val Ser Asn Glu Phe His Gly Asn	
265 270 275	

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 295 300 305

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 Glu Leu Ala Ala Val Lys Ser Val Arg Lys Gly Glu Pro Thr Glu
 310 315 320 325

gag gag atc gac acc ctt cca cgg ttg gcc acc aaa tgg gtc gca caa 1123
 Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr Lys Trp Val Ala Gln
 330 335 340

aac cca caa ccg ctg cca ctg gga gag gtt gac tac aag cgc 1165
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 345 350 355

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 35 40 45

Gly Val Pro Glu Glu Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp
 50 55 60

Val Asp Ile Arg Asn Glu Asp Gly Asp Thr Pro Leu His Val His Ser
 65 70 75 80

His Asp Trp Asn Leu Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp
 85 90 95

Val Cys Ala Val Asn Asn Glu Gly Glu Ser Val Ala Tyr Ser Ala Ala
 100 105 110

Phe Phe Pro Glu Asn Leu Lys Lys Leu Ile Asp Ala Gly Ala Asp Pro
 115 120 125

Tyr Ser Arg Ala Asn Asp Gly Thr Thr Pro Leu Met Arg Val Ile Arg
 130 135 140

Ser Ala Asp Thr Gly Gln Ile Ile Glu Leu Ala Glu Ile Thr Lys Leu
 145 150 155 160

Leu Ser Gly Thr Glu Phe Thr Asp Ala Glu Phe Arg Glu Thr Gln Glu
 165 170 175

Arg Ile Ile Ala Met Gly Glu Arg Phe Glu Asp Val Arg Glu Val Tyr
 180 185 190
 Asn Glu Glu Ser Val Asp Gln Ala Ser Ala Asp Met Ile Trp Leu Tyr
 195 200 205
 Asp Arg Phe Asp Ile Pro Glu Glu Leu Arg Ala Asn Thr Pro Ile Leu
 210 215 220
 His Asp Gly Val Ser Pro Ile Glu Leu Pro Gly Asp Thr Trp Gln Glu
 225 230 235 240
 Gln Phe Ile Glu Gly Tyr Asp Leu Leu Val Pro Ala Met Gly Lys Ala
 245 250 255
 Lys Ser Leu Gln Gly Glu Ala Ile Arg Ile Ala Gly Arg Val Ser Asn
 260 265 270
 Glu Phe His Gly Asn Gly Gly Val Asn Trp Asp Lys Asp Phe Lys Arg
 275 280 285
 Met Ala Lys Ser Leu Asn His Ile Cys Glu Gln Gly Val Pro Leu Gly
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 Glu Pro Glu Leu Glu Glu Leu Ala Ala Ala Val Lys Ser Val Arg Lys
 305 310 315 320
 Gly Glu Pro Thr Glu Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr
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 Tyr Lys Arg
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 <223> RXA01827

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 Met Ser Gln Glu Asp
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 atc act gga aaa gat cga ctc caa gaa ctc atc ggc gct gat tat cgt 163
 Ile Thr Gly Lys Asp Arg Leu Gln Glu Leu Ile Gly Ala Asp Tyr Arg
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 ctg cag tgg atc atc gga cac ggt ggc atg tcc acc gta tgg ctc gca 211
 Leu Gln Trp Ile Ile Gly His Gly Gly Met Ser Thr Val Trp Leu Ala

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Asp	Asp	Val	Val	Asn	Asp	Arg	Glu	Val	Ala	Ile	Lys	Val	Leu	Arg	Pro	
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Glu	Phe	Ser	Asp	Asn	Gln	Glu	Phe	Leu	Asn	Arg	Phe	Arg	Asn	Glu	Ala	
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Gln	Ala	Ala	Glu	Asn	Ile	Asp	Ser	Glu	His	Val	Val	Ala	Thr	Tyr	Asp	
	70				75					80					85	
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Tyr	Arg	Glu	Val	Pro	Asp	Pro	Ala	Gly	His	Thr	Phe	Cys	Phe	Ile	Val	
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Met	Glu	Phe	Val	Arg	Gly	Glu	Ser	Leu	Ala	Asp	Leu	Leu	Glu	Arg	Glu	
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Gly	Arg	Leu	Pro	Glu	Asp	Leu	Ala	Leu	Asp	Val	Met	Glu	Gln	Ala	Ala	
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His	Gly	Leu	Ser	Val	Ile	His	Arg	Met	Asp	Met	Val	His	Arg	Asp	Ile	
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Lys	Pro	Gly	Asn	Met	Leu	Ile	Thr	Ala	Asn	Gly	Ile	Val	Lys	Ile	Thr	
	150				155					160					165	
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ggc	atg	gtg	gtg	ggg	act	gct	caa	tat	gtt	tca	cct	gag	caa	gcc	cag	691
Gly	Met	Val	Val	Gly	Thr	Ala	Gln	Tyr	Val	Ser	Pro	Glu	Gln	Ala	Gln	
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ggc	aag	gaa	gtc	acc	gcg	gct	tct	gat	att	tat	tct	ctc	ggg	gtg	gtc	739
Gly	Lys	Glu	Val	Thr	Ala	Ala	Ser	Asp	Ile	Tyr	Ser	Leu	Gly	Val	Val	
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ggc	tat	gag	atg	atg	gct	ggc	cgc	cgc	ccg	ttc	act	gga	gat	tct	tcg	787
Gly	Tyr	Glu	Met	Met	Ala	Gly	Arg	Arg	Pro	Phe	Thr	Gly	Asp	Ser	Ser	
	215					220					225					
gtg	tct	gtg	gcg	atc	gcg	cac	atc	aac	caa	gct	ccg	ccg	cag	atg	ccc	835
Val	Ser	Val	Ala	Ile	Ala	His	Ile	Asn	Gln	Ala	Pro	Pro	Gln	Met	Pro	
	230				235					240					245	
acc	agc	att	tcg	gca	cag	act	cgc	gag	ttg	att	ggc	att	gcg	ttg	cgc	883
Thr	Ser	Ile	Ser	Ala	Gln	Thr	Arg	Glu	Leu	Ile	Gly	Ile	Ala	Leu	Arg	
				250					255					260		
aag	gat	ccg	ggg	cgc	cgt	ttc	cct	gat	gga	aat	gaa	atg	gcg	cta	gct	931
Lys	Asp	Pro	Gly	Arg	Arg	Phe	Pro	Asp	Gly	Asn	Glu	Met	Ala	Leu	Ala	
			265					270					275			

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 Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro Gln Pro Arg Thr Ser
 280 285 290

gcg atg atg gcg cag gcg gag gcg ccg tcg cca agc gaa tca acg gcg 1027
 Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro Ser Glu Ser Thr Ala
 295 300 305

atg ctg ggc agg gtg gcc cgg cct gca aca atc acc caa gaa gcg gcc 1075
 Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile Thr Gln Glu Ala Ala
 310 315 320 325

ccg aaa cgc ggt tcc ggc att ggc att ggt ctg ttc atc gca gct ttg 1123
 Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu Phe Ile Ala Ala Leu
 330 335 340

ctt gcc gtg att att ggc gcg gtg atc tat gcg ggc acc acc gga att 1171
 Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala Gly Thr Thr Gly Ile
 345 350 355

ttg ttc aac gac act ccg gaa gaa acc acc aca cct gaa acc att acg 1219
 Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr Pro Glu Thr Ile Thr
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gaa aca tac acc cca acc gtg gag gaa acc acc tct cag tgg gta ccg 1267
 Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr Ser Gln Trp Val Pro
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cca acg cct cca aca cgg tca aca ttc acc gaa cct gaa aca act tca 1315
 Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu Pro Glu Thr Thr Ser
 390 395 400 405

cac cgt ccg acg aca agt gaa gag agc aca tcc gag gaa cca acc acg 1363
 His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser Glu Glu Pro Thr Thr
 410 415 420

gaa gct cca aca agt agc cga act gtg cct caa atc cct acc tct aca 1411
 Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln Ile Pro Thr Ser Thr
 425 430 435

cct agg acg agt gct agc gtt cca gtt gag act aat gca ccg gct gat 1459
 Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr Asn Ala Pro Ala Asp
 440 445 450

gat tta atc gac gcc gta aat ggc cta ttg gat gta gga gga gcg cag 1507
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tgaccttcgt gatcgctgat cgc 1530

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<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 Thr Val Trp Leu Ala Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile
 35 40 45
 Lys Val Leu Arg Pro Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg
 50 55 60
 Phe Arg Asn Glu Ala Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val
 65 70 75 80
 Val Ala Thr Tyr Asp Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr
 85 90 95
 Phe Cys Phe Ile Val Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp
 100 105 110
 Leu Leu Glu Arg Glu Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val
 115 120 125
 Met Glu Gln Ala Ala His Gly Leu Ser Val Ile His Arg Met Asp Met
 130 135 140
 Val His Arg Asp Ile Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly
 145 150 155 160
 Ile Val Lys Ile Thr Asp Phe Gly Ile Ala Lys Ala Ala Ala Ala Val
 165 170 175
 Pro Leu Thr Arg Thr Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser
 180 185 190
 Pro Glu Gln Ala Gln Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr
 195 200 205
 Ser Leu Gly Val Val Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe
 210 215 220
 Thr Gly Asp Ser Ser Val Ser Val Ala Ile Ala His Ile Asn Gln Ala
 225 230 235 240
 Pro Pro Gln Met Pro Thr Ser Ile Ser Ala Gln Thr Arg Glu Leu Ile
 245 250 255
 Gly Ile Ala Leu Arg Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn
 260 265 270
 Glu Met Ala Leu Ala Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro
 275 280 285
 Gln Pro Arg Thr Ser Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro
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 Ser Glu Ser Thr Ala Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile
 305 310 315 320
 Thr Gln Glu Ala Ala Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu
 325 330 335
 Phe Ile Ala Ala Leu Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala

340	345	350
Gly Thr Thr Gly Ile Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr		
355	360	365
Pro Glu Thr Ile Thr Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr		
370	375	380
Ser Gln Trp Val Pro Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu		
385	390	395
Pro Glu Thr Thr Ser His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser		
405	410	415
Glu Glu Pro Thr Thr Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln		
420	425	430
Ile Pro Thr Ser Thr Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr		
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Asn Ala Pro Ala Asp Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp		
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Val Gly Gly Ala Gln		
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<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1231)

<223> RXA00813

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                                     Met Thr Asp Ile Asp
                                     1 5
ctg gtg gtg gaa aac gtc caa agg att atc gcc acc aaa gag aca ccg 163
Leu Val Val Glu Asn Val Gln Arg Ile Ile Ala Thr Lys Glu Thr Pro
                                     10 15 20
ccg acc tct gcg gaa ata gcg agc ctg att cgg gaa caa gca ggc gtg 211
Pro Thr Ser Ala Glu Ile Ala Ser Leu Ile Arg Glu Gln Ala Gly Val
                                     25 30 35
atc agt aac gag gac atc gtg atg gtg ttg cgt cga ctg cgc agt gat 259
Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg Arg Leu Arg Ser Asp
                                     40 45 50
tct gtg ggc gtg gga ccg ttg gaa tct ctg ctt gcg ctt cct ggc gtg 307
Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu Ala Leu Pro Gly Val
                                     55 60 65
acg gat gtg ttg gtt aat gcc cat gac agc gtg tgg att gat cgc ggt 355

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Gln	Gly	Val	Glu	Lys	Val	Asp	Met	Asp	Leu	Gly	Ser	Glu	Glu	Ala	Val			
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Asp	Ala	Gln	Pro	Phe	Ala	Asp	Gly	Arg	Ile	Thr	Arg	Asp	Asp	Gly	Ser			
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Val	Leu	Arg	Ile	His	Ala	Val	Leu	Ala	Pro	Leu	Ala	Glu	Ser	Gly	Thr			
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tgc	atc	agt	gtg	cga	gta	ctg	cgt	caa	gca	cgg	ctg	agc	ctt	gat	gat		595	
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Leu	Ile	Gln	Ser	Gly	Thr	Val	Pro	Glu	Asp	Ile	Ala	Pro	Ala	Leu	Arg			
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aac	atc	atc	aat	caa	cgg	cgc	tcg	ttc	ctt	gtt	gtc	ggt	ggc	acc	ggc		691	
Asn	Ile	Ile	Asn	Gln	Arg	Arg	Ser	Phe	Leu	Val	Val	Gly	Gly	Thr	Gly			
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aca	ggg	aaa	acc	aca	ttg	ctg	tcc	gcg	atg	ctc	acc	gaa	gtt	ccc	gct		739	
Thr	Gly	Lys	Thr	Thr	Leu	Leu	Ser	Ala	Met	Leu	Thr	Glu	Val	Pro	Ala			
		200					205					210						
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Asp	Gln	Arg	Ile	Ile	Cys	Ile	Glu	Asp	Thr	Ala	Glu	Leu	His	Pro	Gly			
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				250					255					260				
agg	cct	gac	cgg	att	gtc	gtc	gga	gag	att	cgc	ggt	gcg	gaa	gtc	gtg		931	
Arg	Pro	Asp	Arg	Ile	Val	Val	Gly	Glu	Ile	Arg	Gly	Ala	Glu	Val	Val			
			265					270					275					
gat	ctt	ttg	gct	gcg	atg	aat	acc	gga	cac	gac	ggc	ggt	gct	ggc	acc		979	
Asp	Leu	Leu	Ala	Ala	Met	Asn	Thr	Gly	His	Asp	Gly	Gly	Ala	Gly	Thr			
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att	cac	gcg	aac	tcc	atc	tct	gaa	gtt	ccc	gcg	cgc	atg	gaa	gct	ctt		1027	
Ile	His	Ala	Asn	Ser	Ile	Ser	Glu	Val	Pro	Ala	Arg	Met	Glu	Ala	Leu			
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gcg	gcg	acc	ggc	gga	ttg	gac	cgc	atg	gca	ttg	cat	tct	caa	ctc	gcg		1075	
Ala	Ala	Thr	Gly	Gly	Leu	Asp	Arg	Met	Ala	Leu	His	Ser	Gln	Leu	Ala			

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Ala Ala Val Asp Ile Val Leu Val Met Lys His Thr Pro Phe Gly Arg				
	330	335	340	
agg cta gct caa ctc ggg gtg ctc cgc gga aat cct gtg acc acg cag				1171
Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn Pro Val Thr Thr Gln				
	345	350	355	
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Val Val Trp Asp Leu Asp His Gly Met His Glu Gly Ser Glu Glu Ala				
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Trp Phe Met Pro				
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<400> 62

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Glu Gln Ala Gly Val Ile Ser Asn Glu Asp Ile Val Met Val Leu Arg			
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Arg Leu Arg Ser Asp Ser Val Gly Val Gly Pro Leu Glu Ser Leu Leu			
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Ala Leu Pro Gly Val Thr Asp Val Leu Val Asn Ala His Asp Ser Val			
	65	70	75
Trp Ile Asp Arg Gly Gln Gly Val Glu Lys Val Asp Met Asp Leu Gly			
	85	90	95
Ser Glu Glu Ala Val Arg Arg Leu Ala Thr Arg Leu Ala Leu Thr Cys			
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Gly Arg Arg Leu Asp Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr			
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Arg Asp Asp Gly Ser Val Leu Arg Ile His Ala Val Leu Ala Pro Leu			
	130	135	140
Ala Glu Ser Gly Thr Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg			
	145	150	155
Leu Ser Leu Asp Asp Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile			
	165	170	175
Ala Pro Ala Leu Arg Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val			
	180	185	190

Val Gly Gly Thr Gly Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu
 195 200 205

Thr Glu Val Pro Ala Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala
 210 215 220

Glu Leu His Pro Gly His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln
 225 230 235 240

Ala Asn Val Glu Gly Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys
 245 250 255

Gln Ser Leu Arg Met Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg
 260 265 270

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 275 280 285

Gly Gly Ala Gly Thr Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala
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His Ser Gln Leu Ala Ala Ala Val Asp Ile Val Leu Val Met Lys His
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Thr Pro Phe Gly Arg Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn
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 <223> RXA01826

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 Val Thr Phe Val Ile
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 Ala Asp Arg Tyr Glu Leu Asp Ala Val Ile Gly Ser Gly Gly Met Ser
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 Glu Val Phe Ala Ala Thr Asp Thr Leu Ile Gly Arg Glu Val Ala Val
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aag atg ctg cgc atc gac ctt gcg aaa gat ccc aat ttc cga gaa cgc	259
Lys Met Leu Arg Ile Asp Leu Ala Lys Asp Pro Asn Phe Arg Glu Arg	
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Phe Arg Arg Glu Ala Gln Asn Ser Gly Arg Leu Ser His Ser Ser Ile	
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Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys Asp Gly Thr Ser Val	
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ccc tac att gtg atg gaa cgc gtg cag ggt cga aac ctg cgc gaa gtt	403
Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg Asn Leu Arg Glu Val	
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Val Thr Glu Asp Gly Val Phe Thr Pro Val Glu Ala Ala Asn Ile Leu	
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Ile Pro Val Cys Glu Ala Leu Gln Ala Ser His Asp Ala Gly Ile Ile	
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His Arg Asp Val Lys Pro Ala Asn Ile Met Ile Thr Asn Thr Gly Gly	
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Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala Val Asn Asp Ser Thr	
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Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly Thr Ala Gln Tyr Leu	
170 175 180	
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Ser Pro Glu Gln Ala Arg Gly Lys Pro Ala Asp Ala Arg Ser Asp Ile	
185 190 195	
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Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val Thr Gly Lys Pro Pro	
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Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr Gln His Val Gln Glu	
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Asp Pro Thr Pro Pro Ser Asp Phe Ile Ala Asp Leu Thr Pro Thr Ser	
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Ala Val Asn Val Asp Ala Val Val Leu Thr Ala Met Ala Lys His Pro	
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Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala Ala Asp Leu Gly Arg	
265 270 275	

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Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg Ala His Val Glu Thr	
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Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe Ser Thr Arg Thr Ser	
295 300 305	
acc caa gtg gcc ccc gcc gca ggc gtg gct gcg gcc agt acg ggg tca	1075
Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala Ala Ser Thr Gly Ser	
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Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly Leu Thr Ala Leu Ala	
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Ile Val Leu Ser Leu Gly Val Val Gly Val Ala Gly Ala Phe Thr Tyr	
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Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr Ser Ala Ile Pro Asn	
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Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser Ala Asp Val Ala Glu	
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Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly Ser Glu Ile Arg Gln	
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Gln Glu Val Val Val Gly Ser Ser Val Ser Leu Thr Met Ser Ser Gly	
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Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly Met Asn Trp Ser Gln	
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<212> PRT

<213> Corynebacterium glutamicum

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Ala	Asp	Val	Ala	Glu	Gly	Leu	Val	Ile	Arg	Ala	Asn	Pro	Ser	Val	Gly		
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Met Asn Trp Ser Gln Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn
515 520 525

Pro Thr Ala Ser Tyr Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu
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Ser Val Ser Ser Gln Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr
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Met Ser Thr Glu Gln Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr
580 585 590

Ala Pro Asp Gln Ser Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala
595 600 605

Leu Val Asp Gln Asn Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr
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Leu Ala Ala Leu Val Gln
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Met Ser Thr Val Tyr
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Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met Ala Leu Lys Val Met	
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Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg Gln Arg Ser Arg Arg	
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Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro Asn Leu Val Asn Val	
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Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr Leu Val Met Glu Leu	
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Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala Glu Arg Gly Pro Met	
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Pro Pro His Ala Ala Val Gly Val Met Arg Gly Val Leu Thr Gly Leu	
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Ala Ala Ala His Arg Ala Gly Met Val His Arg Asp Ile Lys Pro Asp	
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Asn Val Leu Ile Asn Ser Asp His Gln Val Lys Leu Ser Asp Phe Gly	
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Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln Asp Asn Gln Ile Val	
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Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu Phe Leu Ser Ala Leu	
230 235 240 245	
gaa gat gtc gca aca gag ttg agc ttg ccg gct ttc cgg gtc cct gtg	883

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Thr	Val	Ser	Asn	Arg	Ser	Lys	Leu	Lys	Leu	Thr	Leu	Trp	Ser	Ile	Phe		
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Gln	Ala	Val	Ala	Val	Val	Glu	Glu	Ala	Gly	Phe	Val	Ala	Val	Ala	Glu		
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Pro	Gln	Tyr	Asp	Asn	Glu	Val	Pro	Thr	Gly	Ser	Ile	Ile	Gly	Thr	Glu		
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Pro	Ser	Phe	Gly	Glu	Arg	Leu	Pro	Arg	Gly	Glu	Asp	Val	Ser	Val	Leu		
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<213> *Corynebacterium glutamicum*

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Ser	Ser	Leu	Ile	Asp	Gly	Val	Pro	Ser	Leu	Ile	Asp	Glu	Leu	Val	Ala
	210					215					220				
Thr	Ala	Thr	Ser	Ile	Asn	Pro	Glu	Asp	Arg	Phe	Asp	Asp	Ser	Gly	Glu
225					230					235					240
Phe	Leu	Ser	Ala	Leu	Glu	Asp	Val	Ala	Thr	Glu	Leu	Ser	Leu	Pro	Ala
				245					250					255	
Phe	Arg	Val	Pro	Val	Pro	Val	Asn	Ser	Ala	Ala	Asn	Arg	Ala	Asn	Ala
			260					265					270		
Gln	Val	Pro	Asp	Ala	Gln	Pro	Thr	Asp	Met	Phe	Thr	Thr	His	Ile	Pro
		275					280					285			
Lys	Thr	Pro	Glu	Pro	Asp	His	Thr	Ala	Ile	Ile	Pro	Val	Ala	Ser	Ala
	290					295					300				

Asn Glu Thr Ser Ile Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala
 305 310 315 320
 Gln Asn Pro Leu Gln Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro
 325 330 335
 Pro Asp Thr Ala Leu Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp
 340 345 350
 Glu Pro Glu Ile Asn Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr
 355 360 365
 Leu Trp Ser Ile Phe Val Val Ala Val Ile Ala Ala Val Ala Val Gly
 370 375 380
 Gly Trp Trp Phe Gly Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu
 385 390 395 400
 Gly Met Asp Glu Val Gln Ala Val Ala Val Val Glu Glu Ala Gly Phe
 405 410 415
 Val Ala Val Ala Glu Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser
 420 425 430
 Ile Ile Gly Thr Glu Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu
 435 440 445
 Asp Val Ser Val Leu Val Ser Gln Gly Arg Pro Val Val Pro Asp Leu
 450 455 460
 Ser Glu Asp Arg Ser Leu Ser Thr Val Arg Glu Glu Leu Glu Gln Arg
 465 470 475 480
 Thr Phe Val Trp Val Asp Gly Pro Gly Glu Tyr Ser Asp Asp Val Pro
 485 490 495
 Glu Gly Gln Val Val Ser Phe Thr Pro Ser Ser Gly Thr Gln Leu Asp
 500 505 510
 Val Gly Glu Thr Val Gln Ile His Leu Ser Arg Gly Pro Ala Pro Val
 515 520 525
 Glu Ile Pro Asp Val Ser Gly Met Gly Val Asp Gln Ala Thr Arg Val
 530 535 540
 Leu Glu Arg Ala Gly Leu Ser Val Glu Arg Thr Glu Glu Gly Phe Asp
 545 550 555 560
 Ala Glu Thr Pro Asn Gly Asp Val Tyr Gly Thr Ser Pro Lys Val Ser
 565 570 575
 Thr Glu Val Lys Arg Gly Thr Ser Val Val Leu Gln Val Ser Asn Ala
 580 585 590
 Ile Ser Val Pro Asp Val Val Gly Met Thr Lys Asp Glu Ala Thr Ala
 595 600 605
 Ala Leu Ala Glu Glu Gly Leu Val Val Ala Ser Thr Ser Ile Ile Pro
 610 615 620
 Gly Glu Ala Ala Ser Ser Ala Asp Ala Val Val Thr Val Glu Pro Glu

625	630	635	640
Ser Gly Ser Arg Val Asp Pro Ala His Pro Gln Val Ser Leu Gly Leu	645	650	655
Ala Gly Glu Ile Gln Val Pro Ser Val Val Gly Arg Lys Val Ser Asp	660	665	670
Ala Arg Ser Ile Leu Glu Glu Ala Gly Leu Thr Leu Thr Thr Asp Ala	675	680	685
Asp Asp Asn Asp Arg Ile Tyr Ser Gln Thr Pro Arg Ala Arg Ser Glu	690	695	700
Val Ser Val Gly Gly Glu Val Thr Val Arg Ala Phe	705	710	715

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 <211> 549
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(526)
 <223> RXA00319

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 aattgttttc gtatgcaccg gaaacatttg ccgatccccc atg tcg gaa gtc atc 115
 Met Ser Glu Val Ile
 1 5
 gcg aag gca aaa gcg gaa gaa gct ggc ttg gaa gac aac gtc att ttc 163
 Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu Asp Asn Val Ile Phe
 10 15 20
 tcc tcc tgt ggc atg ggc aat tgg cac gtt ggc caa cct gct gac aag 211
 Ser Ser Cys Gly Met Gly Asn Trp His Val Gly Gln Pro Ala Asp Lys
 25 30 35
 cga gct ctc gcg gaa ctg aaa tca gcc ggt tac aac gcc gac acc cac 259
 Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr Asn Gly Asp Thr His
 40 45 50
 cgc gca gca caa ctt ggt ccc gag cac atg cgc gca gat ctc ttc gtc 307
 Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg Ala Asp Leu Phe Val
 55 60 65
 gcg cta gat tcc ggc cac gcc ggt gag ctc gcc gca acg ggt gtt ccc 355
 Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala Ala Thr Gly Val Pro
 70 75 80 85
 aac gac aaa atc cgc ctc atg cgt tcc ttc gac cca gag tcc aac ccc 403
 Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp Pro Glu Ser Asn Pro
 90 95 100
 acc gac gat gtc gca gac cct tac tac ggc aca tcc cag gat ttc gtg 451
 Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr Ser Gln Asp Phe Val

105 110 115

ctc acc cgt gaa aac atc gaa gat gct atg ccg ggc ctt ttg gag tgg 499
 Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro Gly Leu Leu Glu Trp
 120 125 130

gtc aga gat cac atc cgc act gat tct taggtctttg agctaaaaag 546
 Val Arg Asp His Ile Arg Thr Asp Ser
 135 140

tcc 549

<210> 68
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 68
 Met Ser Glu Val Ile Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu
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Asp Asn Val Ile Phe Ser Ser Cys Gly Met Gly Asn Trp His Val Gly
 20 25 30

Gln Pro Ala Asp Lys Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr
 35 40 45

Asn Gly Asp Thr His Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg
 50 55 60

Ala Asp Leu Phe Val Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala
 65 70 75 80

Ala Thr Gly Val Pro Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp
 85 90 95

Pro Glu Ser Asn Pro Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr
 100 105 110

Ser Gln Asp Phe Val Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro
 115 120 125

Gly Leu Leu Glu Trp Val Arg Asp His Ile Arg Thr Asp Ser
 130 135 140

<210> 69
 <211> 726
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(703)
 <223> RXA01272

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 aacaccgaac taaccaccac cgatgcttcc aaggccaaca atg agc aat agc ttc 115

	Met	Ser	Asn	Ser	Phe	
	1				5	
act att ctc act gtc tgt act gga aac att tgc cgc tcc ccg tta gct						163
Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys Arg Ser Pro Leu Ala						
	10			15	20	
aag cag cta ctt gaa ctt gag ctt ccg ggg gca gat ata atc cgc gtt						211
Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala Asp Ile Ile Arg Val						
	25			30	35	
gat tcc gcc ggt gtt cag gcg atg gtt gat tcg cct atg ccg gag caa						259
Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser Pro Met Pro Glu Gln						
	40			45	50	
tct tta gaa atc gca cgt aaa cag ggc ata gaa aac cct gag gag cac						307
Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu Asn Pro Glu Glu His						
	55			60	65	
cga gct aag cag att act gag gag ctt gta aac caa tct gat ctg att						355
Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn Gln Ser Asp Leu Ile						
	70			75	80	85
ctt gcg atg gat cgg ggg cat cga aaa tcc att gtc cag cta agc ccg						403
Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile Val Gln Leu Ser Pro						
	90			95	100	
cgt gca acc cgt aag gtt ttc act gtt gtt gat ctt gcc agg tta att						451
Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp Leu Ala Arg Leu Ile						
	105			110	115	
gag gca aca act gat gct gat ctg cag gaa gag ctc aat ctg gca ggg						499
Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu Leu Asn Leu Ala Gly						
	120			125	130	
gat tcc gtg atc gat agg ctg cat gcg aca gtt gag gct gct cgt ctt						547
Asp Ser Val Ile Asp Arg Leu His Ala Thr Val Glu Ala Ala Arg Leu						
	135			140	145	
agc cgc agt gaa ttg aat cct ctg gat aac ctc gca gat gaa gat att						595
Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu Ala Asp Glu Asp Ile						
	150			155	160	165
gtt gac ccg tac gga aag agt caa tcg gtt tat gag gca tcg gcg agt						643
Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr Glu Ala Ser Ala Ser						
	170			175	180	
cag cta att cca gct att cgt ttg att gct tct tat ttg aac aaa gca						691
Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser Tyr Leu Asn Lys Ala						
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ctg gag tct gcg taatggcgag gaagtatcgg gtg						726
Leu Glu Ser Ala						
	200					

<210> 70

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Arg Ser Pro Leu Ala Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala
 20 25 30

Asp Ile Ile Arg Val Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser
 35 40 45

Pro Met Pro Glu Gln Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu
 50 55 60

Asn Pro Glu Glu His Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn
 65 70 75 80

Gln Ser Asp Leu Ile Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile
 85 90 95

Val Gln Leu Ser Pro Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp
 100 105 110

Leu Ala Arg Leu Ile Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu
 115 120 125

Leu Asn Leu Ala Gly Asp Ser Val Ile Asp Arg Leu His Ala Thr Val
 130 135 140

Glu Ala Ala Arg Leu Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu
 145 150 155 160

Ala Asp Glu Asp Ile Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr
 165 170 175

Glu Ala Ser Ala Ser Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser
 180 185 190

Tyr Leu Asn Lys Ala Leu Glu Ser Ala
 195 200

<210> 71

<211> 1476

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1453)

<223> RXA01830

<400> 71

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atatccgtat tggctcgtaga gcagtgagggc ttgttccctg atg ttg aaa ctt aaa 115
 Met Leu Lys Leu Lys
 1 5

tat gcg gtg gca tct gac cga ggg tta gtg cgc ggg aac aat gag gat 163
 Tyr Ala Val Ala Ser Arg Gly Leu Val Arg Gly Asn Asn Glu Asp
 10 15 20

tcc gct tac gct ggc ccg cat ttg ttg gcg ctg gct gat ggt atg ggc	211
Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu Ala Asp Gly Met Gly	
25 30 35	
ggc cat gct gct ggt gag atc gct tcc caa acc atg atc aac cat ttg	259
Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr Met Ile Asn His Leu	
40 45 50	
cgt gcg ctt gat gtt gat cct ggt gat aac gat atg ttg gcg ctg gtg	307
Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp Met Leu Ala Leu Val	
55 60 65	
ggc atg gtg gca ggc gaa gcc aac gcg gcg att gct gag ggc atc gcc	355
Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile Ala Glu Gly Ile Ala	
70 75 80 85	
gaa gac ccg gcg cgc gac ggc atg ggc act acg ttg acg gcg ttc atg	403
Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr Leu Thr Ala Phe Met	
90 95 100	
ttt aac ggg cgt gac ctg gca atg tgc cac gtc ggc gat agt cgt ggt	451
Phe Asn Gly Arg Asp Leu Ala Met Cys His Val Gly Asp Ser Arg Gly	
105 110 115	
tat gtg ctt cgc gac gat aag ttg gta cag gtt aca gtc gac gat act	499
Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val Thr Val Asp Asp Thr	
120 125 130	
ttt gtg cag tcg ttg gtc gct gag ggc aag ctt gat cca gaa gat gtt	547
Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu Asp Pro Glu Asp Val	
135 140 145	
tca act cac cct cag cgt tct ttg att ctg aag gct tac acc ggc cat	595
Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys Ala Tyr Thr Gly His	
150 155 160 165	
cct gtg gag ccc act ctg gag caa ttc ccg gcc ttg cct ggg gat cgt	643
Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala Leu Pro Gly Asp Arg	
170 175 180	
ttg ttg ttg tgc tct gat ggt cta tca gat ccg gtt aca cac tcc acg	691
Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro Val Thr His Ser Thr	
185 190 195	
att gaa gaa aca gtg cgt gta ggc acc ccg cag gat gcg tcc acc aag	739
Ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln Asp Ala Ser Thr Lys	
200 205 210	
ttg gtg gag ttg gcg ctg cgt tct ggc ggt ccg gac aat gtg acg gtc	787
Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro Asp Asn Val Thr Val	
215 220 225	
att gtg gcc gat gtt gta gaa gtc acc gag gcg gaa gca gca gcg gaa	835
Ile Val Ala Asp Val Val Glu Val Thr Glu Ala Glu Ala Ala Ala Glu	
230 235 240 245	
gca tca gtg cct gtc acg gct ggt gcg ctc aat ggt gag cag cct gaa	883
Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn Gly Glu Gln Pro Glu	
250 255 260	

gat ccg cgg cct gat acc gct gcg gga cgc gct gcg gcg atc aca cgg 931
Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala Ala Ile Thr Arg
265 270 275

cga gct caa gtg att gat ccg gca cca aag ata tct gat gct gga acg 979
Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile Ser Asp Ala Gly Thr
280 285 290

gag gat att ccc aca att gag gag cca cca gag aaa agt tcc agc aaa 1027
Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu Lys Ser Ser Ser Lys
295 300 305

ctt gcg gta ttg atc gta gcc ctg gtc atc ctc atc ggt gta gtt gcc 1075
Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu Ile Gly Val Val Ala
310 315 320 325

gca gga tgg tgg ggc tac tcc cgt att gac agc act ttt tac gtc gcg 1123
Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser Thr Phe Tyr Val Ala
330 335 340

gtc aat gat gag gaa gcc atc acc gtg gaa cac ggt gtg gat tac cgc 1171
Val Asn Asp Glu Glu Ala Ile Thr Val Glu His Gly Val Asp Tyr Arg
345 350 355

atc ttt ggc aag gat tta cat tcg caa ttc cag gtg gcg tgc ctg aat 1219
Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln Val Ala Cys Leu Asn
360 365 370

gaa gct ggc acc ttg tca ctc aag gaa tcc tgt gaa aac ggt acg tct 1267
Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys Glu Asn Gly Thr Ser
375 380 385

ttc aaa ttg gat gat tta ccg gca tct gtt cgc ggt agt gtc gca gga 1315
Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg Gly Ser Val Ala Gly
390 395 400 405

tta ccg tct ggg tcg tat gac gag gtc cag gcg caa atg caa cgg ctg 1363
Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala Gln Met Gln Arg Leu
410 415 420

gct gct caa gct ttg cca gtg tgc gtg aac tta gaa gta aca acc ggt 1411
Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu Glu Val Thr Thr Gly
425 430 435

ggc gat aga aac gaa ccc gga gtc aat tgt agg gag gtc tca 1453
Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg Glu Val Ser
440 445 450

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<210> 72

<211> 451

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

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Gly Asn Asn Glu Asp Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu

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Ala	Asp	Gly 35	Met	Gly	Gly	His	Ala 40	Ala	Gly	Glu	Ile	Ala 45	Ser	Gln	Thr
Met	Ile 50	Asn	His	Leu	Arg	Ala 55	Leu	Asp	Val	Asp	Pro 60	Gly	Asp	Asn	Asp
Met 65	Leu	Ala	Leu	Val	Gly 70	Met	Val	Ala	Gly	Glu 75	Ala	Asn	Ala	Ala	Ile 80
Ala	Glu	Gly	Ile	Ala 85	Glu	Asp	Pro	Ala	Arg 90	Asp	Gly	Met	Gly	Thr 95	Thr
Leu	Thr	Ala	Phe 100	Met	Phe	Asn	Gly	Arg 105	Asp	Leu	Ala	Met	Cys 110	His	Val
Gly	Asp	Ser 115	Arg	Gly	Tyr	Val	Leu 120	Arg	Asp	Asp	Lys	Leu 125	Val	Gln	Val
Thr	Val 130	Asp	Asp	Thr	Phe	Val 135	Gln	Ser	Leu	Val	Ala 140	Glu	Gly	Lys	Leu
Asp 145	Pro	Glu	Asp	Val	Ser 150	Thr	His	Pro	Gln	Arg 155	Ser	Leu	Ile	Leu	Lys 160
Ala	Tyr	Thr	Gly	His 165	Pro	Val	Glu	Pro	Thr 170	Leu	Glu	Gln	Phe	Pro 175	Ala
Leu	Pro	Gly	Asp 180	Arg	Leu	Leu	Leu	Cys 185	Ser	Asp	Gly	Leu	Ser 190	Asp	Pro
Val	Thr 195	His	Ser	Thr	Ile	Glu	Glu 200	Thr	Val	Arg	Val	Gly 205	Thr	Pro	Gln
Asp 210	Ala	Ser	Thr	Lys	Leu	Val 215	Glu	Leu	Ala	Leu	Arg 220	Ser	Gly	Gly	Pro
Asp 225	Asn	Val	Thr	Val	Ile 230	Val	Ala	Asp	Val	Val 235	Glu	Val	Thr	Glu	Ala 240
Glu	Ala	Ala	Ala	Glu 245	Ala	Ser	Val	Pro	Val 250	Thr	Ala	Gly	Ala	Leu 255	Asn
Gly	Glu	Gln	Pro 260	Glu	Asp	Pro	Arg	Pro 265	Asp	Thr	Ala	Ala	Gly	Arg 270	Ala
Ala	Ala	Ile 275	Thr	Arg	Arg	Ala	Gln 280	Val	Ile	Asp	Pro	Ala 285	Pro	Lys	Ile
Ser 290	Asp	Ala	Gly	Thr	Glu	Asp 295	Ile	Pro	Thr	Ile	Glu 300	Glu	Pro	Pro	Glu
Lys 305	Ser	Ser	Ser	Lys	Leu 310	Ala	Val	Leu	Ile	Val 315	Ala	Leu	Val	Ile	Leu 320
Ile	Gly	Val	Val	Ala 325	Ala	Gly	Trp	Trp	Gly 330	Tyr	Ser	Arg	Ile	Asp 335	Ser
Thr	Phe	Tyr	Val 340	Ala	Val	Asn	Asp 345	Glu	Glu	Ala	Ile	Thr	Val 350	Glu	His

Gly Val Asp Tyr Arg Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln
 355 360 365
 Val Ala Cys Leu Asn Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys
 370 375 380
 Glu Asn Gly Thr Ser Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg
 385 390 395 400
 Gly Ser Val Ala Gly Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala
 405 410 415
 Gln Met Gln Arg Leu Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu
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 Glu Val Thr Thr Gly Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg
 435 440 445
 Glu Val Ser
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<210> 73
 <211> 2199
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2176)
 <223> RXA02747

<400> 73
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 Met Asn Asn Pro Ala
 1 5
 cag ctg cgc caa gat act gaa aag gaa gtc ctg gcg ttg ctg ggc tct 163
 Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu Ala Leu Leu Gly Ser
 10 15 20
 ttg gtt tta ccc gcc ggc acc gcg ctt gcc gcc acc gga tct ttg gcc 211
 Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala Thr Gly Ser Leu Ala
 25 30 35
 agg tcc gaa ctc acg ccg tat tcc gat ttg gac ctc att ttg atc cat 259
 Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp Leu Ile Leu Ile His
 40 45 50
 cca cca gga gcc acc ccg gat ggc gtg gag gat ttg tgg tac ccg att 307
 Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp Leu Trp Tyr Pro Ile
 55 60 65
 tgg gac gca aaa aag cgt ctc gac tac tcc gtg cgc acc cca gat gag 355
 Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val Arg Thr Pro Asp Glu
 70 75 80 85
 tgt gtg gct atg att tct gcg gat tcc act gca gcc ctt gcc atg ctt 403

Cys	Val	Ala	Met	Ile	Ser	Ala	Asp	Ser	Thr	Ala	Ala	Leu	Ala	Met	Leu		
				90					95					100			
gac	ctg	cgg	ttt	gtc	gct	ggc	gat	gag	gat	ctg	tgt	gcc	aaa	acg	cgc	451	
Asp	Leu	Arg	Phe	Val	Ala	Gly	Asp	Glu	Asp	Leu	Cys	Ala	Lys	Thr	Arg		
			105					110					115				
cgg	cgc	atc	gtg	gag	aag	tgg	cgc	cag	gaa	ctc	aac	aaa	aac	ttc	gat	499	
Arg	Arg	Ile	Val	Glu	Lys	Trp	Arg	Gln	Glu	Leu	Asn	Lys	Asn	Phe	Asp		
		120					125					130					
gcc	gtt	gtg	gac	acc	gcg	att	gcc	cgt	tgg	cgc	cgc	tcc	gga	ccc	gtc	547	
Ala	Val	Val	Asp	Thr	Ala	Ile	Ala	Arg	Trp	Arg	Arg	Ser	Gly	Pro	Val		
	135					140					145						
gtg	gca	atg	acg	cgg	cca	gat	ctt	aaa	cac	ggc	agg	gga	ggg	ctg	cgc	595	
Val	Ala	Met	Thr	Arg	Pro	Asp	Leu	Lys	His	Gly	Arg	Gly	Gly	Leu	Arg		
150					155					160					165		
gat	ttc	gaa	ctg	atc	aag	gcc	ctc	gcg	ctc	ggc	cac	cta	tgc	aac	ctt	643	
Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly	His	Leu	Cys	Asn	Leu		
				170					175					180			
cca	cag	ctt	gat	gcg	caa	cac	cag	ctg	ctt	ctc	gac	gcc	cgc	acc	ttg	691	
Pro	Gln	Leu	Asp	Ala	Gln	His	Gln	Leu	Leu	Leu	Asp	Ala	Arg	Thr	Leu		
			185					190					195				
ctg	cac	gtc	cac	gcg	cga	cgc	tcc	cgc	gac	gtc	ctt	gac	ccc	gaa	ttt	739	
Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val	Leu	Asp	Pro	Glu	Phe		
		200					205					210					
gcg	gtg	gat	gtg	gcc	atg	gat	ttg	ggc	ttt	gtt	gac	cgc	tat	cac	ctg	787	
Ala	Val	Asp	Val	Ala	Met	Asp	Leu	Gly	Phe	Val	Asp	Arg	Tyr	His	Leu		
	215					220					225						
ggc	cgg	gag	atc	gcc	gat	gca	gcc	cgc	gcc	att	gat	gat	ggc	ctg	acc	835	
Gly	Arg	Glu	Ile	Ala	Asp	Ala	Ala	Arg	Ala	Ile	Asp	Asp	Gly	Leu	Thr		
230					235					240					245		
acc	gcg	ctg	gcc	acc	gcc	cgt	ggc	att	ttg	cca	cgt	cgc	aca	ggt	ttt	883	
Thr	Ala	Leu	Ala	Thr	Ala	Arg	Gly	Ile	Leu	Pro	Arg	Arg	Thr	Gly	Phe		
				250					255					260			
gca	ttc	agg	aat	gct	tct	cga	cgc	cca	ctt	gat	ctt	gat	gtc	gtc	gac	931	
Ala	Phe	Arg	Asn	Ala	Ser	Arg	Arg	Pro	Leu	Asp	Leu	Asp	Val	Val	Asp		
			265					270					275				
gcc	aac	ggc	acc	atc	gaa	ttg	tcc	aaa	aaa	cca	gat	ctt	aat	gat	ccc	979	
Ala	Asn	Gly	Thr	Ile	Glu	Leu	Ser	Lys	Lys	Pro	Asp	Leu	Asn	Asp	Pro		
		280					285					290					
gca	ctt	cca	ctt	cga	gtg	gcc	gca	gcc	gca	gca	acc	acc	gga	ctt	cgc	1027	
Ala	Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Ala	Ala	Thr	Thr	Gly	Leu	Pro		
	295					300					305						
gtg	gca	gaa	tca	acc	tgg	gtt	cga	ctt	aat	gaa	tgc	ccg	cca	ctt	cct	1075	
Val	Ala	Glu	Ser	Thr	Trp	Val	Arg	Leu	Asn	Glu	Cys	Pro	Pro	Leu	Pro		
310					315					320					325		
gag	cca	tgg	cct	gcc	aat	gca	gca	ggg	gac	ttc	ttt	cgg	att	ctc	tcc	1123	
Glu	Pro	Trp	Pro	Ala	Asn	Ala	Ala	Gly	Asp	Phe	Phe	Arg	Ile	Leu	Ser		

330										335					340					
agt	ccg	aaa	aac	tca	cgc	cga	gtg	gtg	aaa	aat	atg	gat	cgc	cac	gga	1171				
Ser	Pro	Lys	Asn	Ser	Arg	Arg	Val	Val	Lys	Asn	Met	Asp	Arg	His	Gly					
			345						350				355							
ttg	tgg	tcg	cgt	ttt	gtt	cca	gaa	tgg	gac	cgc	atc	aaa	ggg	ctt	atg	1219				
Leu	Trp	Ser	Arg	Phe	Val	Pro	Glu	Trp	Asp	Arg	Ile	Lys	Gly	Leu	Met					
			360				365					370								
ccc	cgt	gaa	ccc	agc	cat	att	tcc	acc	atc	gat	gaa	cat	agt	ctg	aac	1267				
Pro	Arg	Glu	Pro	Ser	His	Ile	Ser	Thr	Ile	Asp	Glu	His	Ser	Leu	Asn					
			375			380					385									
act	gtt	gca	gga	tgt	gcg	cta	gaa	act	gtg	acc	gtc	gcg	cgc	ccc	gat	1315				
Thr	Val	Ala	Gly	Cys	Ala	Leu	Glu	Thr	Val	Thr	Val	Ala	Arg	Pro	Asp					
390					395					400					405					
ctt	tta	gtt	ttg	gga	gcc	ttg	tac	cac	gac	att	ggc	aag	ggc	ttc	ccg	1363				
Leu	Leu	Val	Leu	Gly	Ala	Leu	Tyr	His	Asp	Ile	Gly	Lys	Gly	Phe	Pro					
				410					415					420						
cgt	cca	cac	gaa	caa	gta	ggc	gca	gag	atg	gtg	gcg	agg	gct	gca	agc	1411				
Arg	Pro	His	Glu	Gln	Val	Gly	Ala	Glu	Met	Val	Ala	Arg	Ala	Ala	Ser					
			425					430					435							
cgc	atg	gga	ttg	aac	ctt	cgc	gat	cgt	gcc	agc	gtg	caa	acg	ctg	gtc	1459				
Arg	Met	Gly	Leu	Asn	Leu	Arg	Asp	Arg	Ala	Ser	Val	Gln	Thr	Leu	Val					
		440					445					450								
gcc	gag	cac	acc	gcg	gtg	gcc	aaa	atc	gcc	gcg	cgc	ctt	gat	ccc	tcc	1507				
Ala	Glu	His	Thr	Ala	Val	Ala	Lys	Ile	Ala	Ala	Arg	Leu	Asp	Pro	Ser					
			455			460					465									
tcg	gag	ggc	gcc	gtc	gat	aag	ctg	ctt	gat	gct	gtt	agg	tat	gac	ctg	1555				
Ser	Glu	Gly	Ala	Val	Asp	Lys	Leu	Leu	Asp	Ala	Val	Arg	Tyr	Asp	Leu					
470					475					480					485					
gtg	aca	ttg	aat	ctg	ctt	gag	gtg	cta	aca	gaa	gct	gat	gcg	aaa	gcc	1603				
Val	Thr	Leu	Asn	Leu	Leu	Glu	Val	Leu	Thr	Glu	Ala	Asp	Ala	Lys	Ala					
				490				495						500						
acg	ggg	cct	ggc	gtg	tgg	acg	gcg	cgt	ttg	gag	cat	gcg	ctg	cgg	att	1651				
Thr	Gly	Pro	Gly	Val	Trp	Thr	Ala	Arg	Leu	Glu	His	Ala	Leu	Arg	Ile					
			505					510					515							
gtg	tgc	aag	cgt	gcg	cgt	gat	cgc	ctc	acc	gat	att	cgc	ccg	gtt	gcg	1699				
Val	Cys	Lys	Arg	Ala	Arg	Asp	Arg	Leu	Thr	Asp	Ile	Arg	Pro	Val	Ala					
			520				525					530								
ccg	atg	att	gcg	cca	cgt	agt	gaa	att	ggc	ttg	gtg	gaa	cgc	gat	ggc	1747				
Pro	Met	Ile	Ala	Pro	Arg	Ser	Glu	Ile	Gly	Leu	Val	Glu	Arg	Asp	Gly					
			535			540					545									
gtg	ttc	aca	gtg	caa	tgg	cac	ggc	gaa	gac	tta	cat	cgg	att	ctt	ggc	1795				
Val	Phe	Thr	Val	Gln	Trp	His	Gly	Glu	Asp	Leu	His	Arg	Ile	Leu	Gly					
550					555				560						565					
gta	att	tat	gcc	aaa	gga	tgg	aca	atc	acc	gcg	gcg	cgc	atg	ctg	gcc	1843				
Val	Ile	Tyr	Ala	Lys	Gly	Trp	Thr	Ile	Thr	Ala	Ala	Arg	Met	Leu	Ala					
				570					575					580						

aat ggt caa tgg agt gcg gaa ttt gat gtc cgc gca aac ggc ccc caa 1891
 Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg Ala Asn Gly Pro Gln
 585 590 595

gat ttt gat ccg cag cat ttc ctg cag gca tat caa tcc ggt gtg ttt 1939
 Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr Gln Ser Gly Val Phe
 600 605 610

tcc gag gtt ccc att cca gca ctt ggg ata aca gcc aca ttt tgg cac 1987
 Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr Ala Thr Phe Trp His
 615 620 625

ggg aac act tta gaa gtg cgc act gag ctt cgc aca gga gct att ttt 2035
 Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg Thr Gly Ala Ile Phe
 630 635 640 645

gcc ctg ctc aga aca ttg ccc gat gcc ctc tgg atc aac gct gtg acc 2083
 Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp Ile Asn Ala Val Thr
 650 655 660

cgc ggt gcg acc ctg att atc cag gca gca ctg aag ccc ggc ttc gat 2131
 Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu Lys Pro Gly Phe Asp
 665 670 675

cga gca acg gtg gaa cgc tcc gta gtc agg tcg ttg gca ggt agc 2176
 Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser Leu Ala Gly Ser
 680 685 690

tgacgtgacc tgagcggggg caa 2199

<210> 74

<211> 692

<212> PRT

<213> Corynebacterium glutamicum

<400> 74

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Ala Leu Leu Gly Ser Leu Val Leu Pro Ala Gly Thr Ala Leu Ala Ala
 20 25 30

Thr Gly Ser Leu Ala Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp
 35 40 45

Leu Ile Leu Ile His Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp
 50 55 60

Leu Trp Tyr Pro Ile Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val
 65 70 75 80

Arg Thr Pro Asp Glu Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala
 85 90 95

Ala Leu Ala Met Leu Asp Leu Arg Phe Val Ala Gly Asp Glu Asp Leu
 100 105 110

Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu
 115 120 125

Asn Lys Asn Phe Asp Ala Val Val Asp Thr Ala Ile Ala Arg Trp Arg
 130 135 140
 Arg Ser Gly Pro Val Val Ala Met Thr Arg Pro Asp Leu Lys His Gly
 145 150 155 160
 Arg Gly Gly Leu Arg Asp Phe Glu Leu Ile Lys Ala Leu Ala Leu Gly
 165 170 175
 His Leu Cys Asn Leu Pro Gln Leu Asp Ala Gln His Gln Leu Leu Leu
 180 185 190
 Asp Ala Arg Thr Leu Leu His Val His Ala Arg Arg Ser Arg Asp Val
 195 200 205
 Leu Asp Pro Glu Phe Ala Val Asp Val Ala Met Asp Leu Gly Phe Val
 210 215 220
 Asp Arg Tyr His Leu Gly Arg Glu Ile Ala Asp Ala Ala Arg Ala Ile
 225 230 235 240
 Asp Asp Gly Leu Thr Thr Ala Leu Ala Thr Ala Arg Gly Ile Leu Pro
 245 250 255
 Arg Arg Thr Gly Phe Ala Phe Arg Asn Ala Ser Arg Arg Pro Leu Asp
 260 265 270
 Leu Asp Val Val Asp Ala Asn Gly Thr Ile Glu Leu Ser Lys Lys Pro
 275 280 285
 Asp Leu Asn Asp Pro Ala Leu Pro Leu Arg Val Ala Ala Ala Ala Ala
 290 295 300
 Thr Thr Gly Leu Pro Val Ala Glu Ser Thr Trp Val Arg Leu Asn Glu
 305 310 315 320
 Cys Pro Pro Leu Pro Glu Pro Trp Pro Ala Asn Ala Ala Gly Asp Phe
 325 330 335
 Phe Arg Ile Leu Ser Ser Pro Lys Asn Ser Arg Arg Val Val Lys Asn
 340 345 350
 Met Asp Arg His Gly Leu Trp Ser Arg Phe Val Pro Glu Trp Asp Arg
 355 360 365
 Ile Lys Gly Leu Met Pro Arg Glu Pro Ser His Ile Ser Thr Ile Asp
 370 375 380
 Glu His Ser Leu Asn Thr Val Ala Gly Cys Ala Leu Glu Thr Val Thr
 385 390 395 400
 Val Ala Arg Pro Asp Leu Leu Val Leu Gly Ala Leu Tyr His Asp Ile
 405 410 415
 Gly Lys Gly Phe Pro Arg Pro His Glu Gln Val Gly Ala Glu Met Val
 420 425 430
 Ala Arg Ala Ala Ser Arg Met Gly Leu Asn Leu Arg Asp Arg Ala Ser
 435 440 445

Val Gln Thr Leu Val Ala Glu His Thr Ala Val Ala Lys Ile Ala Ala
450 455 460

Arg Leu Asp Pro Ser Ser Glu Gly Ala Val Asp Lys Leu Leu Asp Ala
465 470 475 480

Val Arg Tyr Asp Leu Val Thr Leu Asn Leu Leu Glu Val Leu Thr Glu
485 490 495

Ala Asp Ala Lys Ala Thr Gly Pro Gly Val Trp Thr Ala Arg Leu Glu
500 505 510

His Ala Leu Arg Ile Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp
515 520 525

Ile Arg Pro Val Ala Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu
530 535 540

Val Glu Arg Asp Gly Val Phe Thr Val Gln Trp His Gly Glu Asp Leu
545 550 555 560

His Arg Ile Leu Gly Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala
565 570 575

Ala Arg Met Leu Ala Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg
580 585 590

Ala Asn Gly Pro Gln Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr
595 600 605

Gln Ser Gly Val Phe Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr
610 615 620

Ala Thr Phe Trp His Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg
625 630 635 640

Thr Gly Ala Ile Phe Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp
645 650 655

Ile Asn Ala Val Thr Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu
660 665 670

Lys Pro Gly Phe Asp Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser
675 680 685

Leu Ala Gly Ser
690

<210> 75

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA02210

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ccatgcgtgt tttcacgcgt attttccata ggagtacatt gtg tcc gta gcg gca 115
                               Val Ser Val Ala Ala
                               1                               5

ggc gac aaa cca aca aat agc cgt caa gaa atc ctc gaa ggt gcc cga 163
Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile Leu Glu Gly Ala Arg
                               10                               15                               20

cgg tgc ttc gct gag cac ggc tat gaa ggc gca acc gta cgc cga ctg 211
Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala Thr Val Arg Arg Leu
                               25                               30                               35

gaa gaa gca aca ggt aaa tca cgc gga gcg atc ttt cat cac ttc ggt 259
Glu Glu Ala Thr Gly Lys Ser Arg Glu Gly Ala Ile Phe His His Phe Gly
                               40                               45                               50

gac aaa gaa aac ctg ttc cta gcc ctc gcg cgg gaa gat gca gcc cgc 307
Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg Glu Asp Ala Ala Arg
                               55                               60                               65

atg gcg gag gtg gtg tct gaa aat ggc ctc gtt gaa gtg atg cga gga 355
Met Ala Glu Val Val Ser Glu Asn Gly Leu Val Glu Val Met Arg Gly
                               70                               75                               80                               85

atg ctg gaa gat cct gaa cga tat gac tgg atg tca gta cgc ctg gag 403
Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met Ser Val Arg Leu Glu
                               90                               95                               100

atc tcc aag cag ctg cgc acc gac ccg gta ttc cgc gca aaa tgg att 451
Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe Arg Ala Lys Trp Ile
                               105                               110                               115

gat cac caa agt gtt cta gac gaa gct gtc cgc gtg cgt ttg tcc cgc 499
Asp His Gln Ser Val Leu Asp Glu Ala Val Arg Val Arg Leu Ser Arg
                               120                               125                               130

aac gtg gat aag gga caa atg cgc act gac gtc ccg atc gaa gtg ctg 547
Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val Pro Ile Glu Val Leu
                               135                               140                               145

cac acc ttc tta gag act gtt ctc gac ggt ttc atc tcc cgt ctt gct 595
His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe Ile Ser Arg Leu Ala
                               150                               155                               160                               165

acc ggc gca tcc aca gaa gga ctg tcc gaa gta ttg gat ctg gtc gag 643
Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val Leu Asp Leu Val Glu
                               170                               175                               180

gga act gtc cgt aaa cgc gac taaacgaccc ctgattcaca ctt 687
Gly Thr Val Arg Lys Arg Asp
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<210> 76

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

Val Ser Val Ala Ala Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile

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Leu Glu Gly Ala Arg Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala	20	25	30
Thr Val Arg Arg Leu Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile	35	40	45
Phe His His Phe Gly Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg	50	55	60
Glu Asp Ala Ala Arg Met Ala Glu Val Val Ser Glu Asn Gly Leu Val	65	70	75
Glu Val Met Arg Gly Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met	85	90	95
Ser Val Arg Leu Glu Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe	100	105	110
Arg Ala Lys Trp Ile Asp His Gln Ser Val Leu Asp Glu Ala Val Arg	115	120	125
Val Arg Leu Ser Arg Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val	130	135	140
Pro Ile Glu Val Leu His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe	145	150	155
Ile Ser Arg Leu Ala Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val	165	170	175
Leu Asp Leu Val Glu Gly Thr Val Arg Lys Arg Asp	180	185	

<210> 77
 <211> 342
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(319)
 <223> RXA00221

<400> 77
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 acggcacgat catgccgaaa gttggatcca aaggatgcac atg aac gca gaa gaa 115
 Met Asn Ala Glu Glu
 1 5
 atc gga atg gcg ctg ctc aac gga cgc aaa gag cta ggc ctt aga caa 163
 Ile Gly Met Ala Leu Leu Asn Gly Arg Lys Glu Leu Gly Leu Arg Gln
 10 15 20
 gga gag ctc gca gac tta gct gga gtt tct gaa cga ttc atc cgc gat 211
 Gly Glu Leu Ala Asp Leu Ala Gly Val Ser Glu Arg Phe Ile Arg Asp
 25 30 35

gtc gaa aag gga aaa act acc gtc cgc ctg gac aaa gtc atc gat gta 259
 Val Glu Lys Gly Lys Thr Thr Val Arg Leu Asp Lys Val Ile Asp Val
 40 45 50

ctc cgc gtc ctt gga ctc gag ctt tct gtt gga att cac gat ccc ctc 307
 Leu Arg Val Leu Gly Leu Glu Leu Ser Val Gly Ile His Asp Pro Leu
 55 60 65

aag gtt aat caa tgacccccac tgccgatatc tgg 342
 Lys Val Asn Gln
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<210> 78

<211> 73

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

Met Asn Ala Glu Glu Ile Gly Met Ala Leu Leu Asn Gly Arg Lys Glu
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Leu Gly Leu Arg Gln Gly Glu Leu Ala Asp Leu Ala Gly Val Ser Glu
 20 25 30

Arg Phe Ile Arg Asp Val Glu Lys Gly Lys Thr Thr Val Arg Leu Asp
 35 40 45

Lys Val Ile Asp Val Leu Arg Val Leu Gly Leu Glu Leu Ser Val Gly
 50 55 60

Ile His Asp Pro Leu Lys Val Asn Gln
 65 70

<210> 79

<211> 594

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(571)

<223> RXN00551

<400> 79

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tagatagggtt atcgaacgga aattacttgg caataccgct atg ctg gca ggc atg 115
 Met Leu Ala Gly Met
 1 5

cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163
 Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
 10 15 20

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
 Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
 25 30 35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259

Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
 40 45 50
 tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
 55 60 65
 gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70 75 80 85
 atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
 90 95 100
 cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca gag 451
 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala Glu
 105 110 115
 atg gct cga ctc ctt gaa atg ctc acc cca gag cag ctg gaa cgt acc 499
 Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu Gln Leu Glu Arg Thr
 120 125 130
 gaa gac ctg gtg gat atc att act gag ctt gca gag gtg tac ggt agc 547
 Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala Glu Val Tyr Gly Ser
 135 140 145
 tgg aaa gag acc gac agc ggt tct taacagtttt ctccatctca act 594
 Trp Lys Glu Thr Asp Ser Gly Ser
 150 155

<210> 80

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Leu Ala Gly Met Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg
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 Val Arg Pro Ala Leu Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser
 20 25 30
 Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu
 35 40 45
 Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp
 50 55 60
 Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu
 65 70 75 80
 Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln
 85 90 95
 Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn
 100 105 110
 Glu Arg Asn Ala Glu Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu
 115 120 125

Gln Leu Glu Arg Thr Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala
 130 135 140

Glu Val Tyr Gly Ser Trp Lys Glu Thr Asp Ser Gly Ser
 145 150 155

<210> 81

<211> 448

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(448)

<223> FRXA00551

<400> 81

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tagatagggtt atcgaacgga aattacttgg caataccgct atg ctg gca ggc atg 115
 Met Leu Ala Gly Met
 1 5

cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163
 Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
 10 15 20

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
 Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
 25 30 35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
 40 45 50

tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
 55 60 65

gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70 75 80 85

atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
 90 95 100

cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca 448
 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala
 105 110 115

<210> 82

<211> 116

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

Met Leu Ala Gly Met Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg

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20	25	30	
Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu			
35	40	45	
Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp			
50	55	60	
Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu			
65	70	75	80
Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln			
85	90	95	
Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn			
100	105	110	
Glu Arg Asn Ala			
115			

<210> 83
 <211> 588
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(565)
 <223> RXA01763

<400> 83
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 agatcgaaac tatttttcag ccagttcaca tggagccact atg acc acc agc aac 115
 Met Thr Thr Ser Asn
 1 5
 ccc acc gcc gag atc att ggc gga cca gaa cga ttc ctc gag gcc gaa 163
 Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg Phe Leu Glu Ala Glu
 10 15 20
 ttg tcc cag cag att caa ttc ctc act gcc cgc gca cga gcc aag gga 211
 Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg Ala Arg Ala Lys Gly
 25 30 35
 tcc gcc aaa gga aac gaa gcc tta gtc gac ctc gga ctt aaa gtt cgc 259
 Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu Gly Leu Lys Val Arg
 40 45 50
 caa tac tcc aca ctg tcc cta gcg gcc agc gga tta aaa cca acc caa 307
 Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly Leu Lys Pro Thr Gln
 55 60 65
 cga gaa ttg gga gca ttt ctc gac cta gac cca agt cag att gtt gcc 355
 Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro Ser Gln Ile Val Ala
 70 75 80 85

ttg gtc gat ttc cta gaa aag cgc gga tta gtg gcc cgg gaa gtt gac 403
 Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val Ala Arg Glu Val Asp
 90 95 100

ccc cgg gat agg cgc tcg aag atc atc atc gcc acc gaa aaa ggt ctg 451
 Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala Thr Glu Lys Gly Leu
 105 110 115

gaa att cac gac gaa gcc acc aaa cgc ctc ctc atc gcc gag ggt gaa 499
 Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu Ile Ala Glu Gly Glu
 120 125 130

tct cta aaa aac ctc acc tcc gac gag caa gaa caa cta agg gaa ctg 547
 Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu Gln Leu Arg Glu Leu
 135 140 145

ctg ctc aaa atc gcc ttt taagtctctt aaccacgccg gcc 588
 Leu Leu Lys Ile Ala Phe
 150 155

<210> 84

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

Met Thr Thr Ser Asn Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg
 1 5 10 15

Phe Leu Glu Ala Glu Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg
 20 25 30

Ala Arg Ala Lys Gly Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu
 35 40 45

Gly Leu Lys Val Arg Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly
 50 55 60

Leu Lys Pro Thr Gln Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro
 65 70 75 80

Ser Gln Ile Val Ala Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val
 85 90 95

Ala Arg Glu Val Asp Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala
 100 105 110

Thr Glu Lys Gly Leu Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu
 115 120 125

Ile Ala Glu Gly Glu Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu
 130 135 140

Gln Leu Arg Glu Leu Leu Leu Lys Ile Ala Phe
 145 150 155

<210> 85

<211> 717

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(694)

<223> RXA02667

<400> 85

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                                         Met Glu Phe Lys Val
                                         1 5

gga gat acc gtc gtt tac ccg cac cac gga gct gca att att tca gcc 163
Gly Asp Thr Val Val Tyr Pro His His Gly Ala Ala Ile Ile Ser Ala
                                         10 15 20

ctg gag cag cgt gaa atg aat ggt gag acg gtg gac tac ctg gtt ctc 211
Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val Asp Tyr Leu Val Leu
                                         25 30 35

cag atc aat cat tcc gat ctc gtc gtt cgc gtt cca gca aag aac gct 259
Gln Ile Asn His Ser Asp Leu Val Val Arg Val Pro Ala Lys Asn Ala
                                         40 45 50

gaa ctc gtt ggc gtg cgt gac gtt gtc ggc gag gag ggc ctg cag aag 307
Glu Leu Val Gly Val Arg Asp Val Val Gly Glu Glu Gly Leu Gln Lys
                                         55 60 65

gtt ttc tct gtt ctt cgt gaa att gac gtc gaa gaa gcc ggc aac tgg 355
Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu Glu Ala Gly Asn Trp
                                         70 75 80 85

tcc cgc cgt tac aag gct aac cag gag cgt ttg gct tcc ggt gac gtg 403
Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu Ala Ser Gly Asp Val
                                         90 95 100

aac aag gtc gct gag gtt gtc cgt gac ctg tgg cgt cgt gat cag gat 451
Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp Arg Arg Asp Gln Asp
                                         105 110 115

cgt ggc ctt tcc gct ggt gag aag cgc atg ctc tcc aag gcg cgt cag 499
Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu Ser Lys Ala Arg Gln
                                         120 125 130

gtt ctt gtt ggt gag ctc gcg ctc gcc gaa acc gtg gac gat gag aag 547
Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr Val Asp Asp Glu Lys
                                         135 140 145

gcg gat gct ttc ctc agc cag gtc gat gag acc att gct cgc cac cgc 595
Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr Ile Ala Arg His Arg
150 155 160 165

gct gac ctg ctc ggc gac gag gaa gag aag aag gac gca ttc gac gac 643
Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys Asp Ala Phe Asp Asp
170 175 180

ttc gac gat tcc gac gtg gat ctt gac gat ctg agc ttc gac gac gaa 691
Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu Ser Phe Asp Asp Glu
185 190 195

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gat tagacgccca tgctgtctac acg
Asp

717

<210> 86
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
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20 25 30
Asp Tyr Leu Val Leu Gln Ile Asn His Ser Asp Leu Val Val Arg Val
35 40 45
Pro Ala Lys Asn Ala Glu Leu Val Gly Val Arg Asp Val Val Gly Glu
50 55 60
Glu Gly Leu Gln Lys Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu
65 70 75 80
Glu Ala Gly Asn Trp Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu
85 90 95
Ala Ser Gly Asp Val Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp
100 105 110
Arg Arg Asp Gln Asp Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu
115 120 125
Ser Lys Ala Arg Gln Val Leu Val Gly Glu Leu Ala Leu Ala Glu Thr
130 135 140
Val Asp Asp Glu Lys Ala Asp Ala Phe Leu Ser Gln Val Asp Glu Thr
145 150 155 160
Ile Ala Arg His Arg Ala Asp Leu Leu Gly Asp Glu Glu Glu Lys Lys
165 170 175
Asp Ala Phe Asp Asp Phe Asp Asp Ser Asp Val Asp Leu Asp Asp Leu
180 185 190
Ser Phe Asp Asp Glu Asp
195

<210> 87
<211> 479
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(456)
<223> RXA00348

<400> 87

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 Thr Arg Glu Arg Leu Glu Asn Ala Gln Tyr Gln Val Gln Arg Asp Arg
 1 5 10 15

gtc agg ggt gcc atg gaa gtc ttt atc gaa gcg gga atc gat ccc ggc 96
 Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
 20 25 30

acc gtg ccg atc atg gaa tgc tgg atc aac aac cgc caa cac aac ttc 144
 Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
 35 40 45

gaa gtg gcc aaa gaa ctt cta gaa aca cac cca gac ctc acc gca gta 192
 Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
 50 55 60

ctc tgt acc gtc gat gca ctg gca ttc ggc gtt ctg gaa tac ctt aaa 240
 Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
 65 70 75 80

agc gta ggt aaa tca gcg cct gca gat cta tcc ctc act ggt ttc gat 288
 Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
 85 90 95

ggc acc cac atg gca ctc gca cgg gat ctc acc acc gtc atc caa ccc 336
 Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
 100 105 110

aac aaa ctc aaa ggg ttc aaa gcc ggc gaa aca ctg ttg aaa atg att 384
 Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
 115 120 125

gac aaa gaa tac gtg gaa cca gaa gtg gaa ttg gaa act tcc ttc cac 432
 Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
 130 135 140

cca ggt tcc acg gtt gcg cca atc taggcttggtg gcacttttcg tgc 479
 Pro Gly Ser Thr Val Ala Pro Ile
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<210> 88

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

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 1 5 10 15

Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
 20 25 30

Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
 35 40 45

Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
 50 55 60

Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
 65 70 75 80
 Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
 85 90 95
 Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
 100 105 110
 Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
 115 120 125
 Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
 130 135 140
 Pro Gly Ser Thr Val Ala Pro Ile
 145 150

<210> 89
 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(544)
 <223> RXA01500

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 Met Ala Thr His Pro
 1 5
 gat att ccc aca gag ttg ctt gaa tct ccg agc tat caa ctt gaa cga 163
 Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser Tyr Gln Leu Glu Arg
 10 15 20
 ctt cga cga cgc act cgt gac cat gtt gag gcc gaa ttg gcc aag cat 211
 Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala Glu Leu Ala Lys His
 25 30 35
 gag acc acg atg agg gaa ttc tgg acg ctt aca tgt ctg gtt cat tcc 259
 Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr Cys Leu Val His Ser
 40 45 50
 gac gct gca agc cag tca gtt ctg tgt gag ctg ctg gcc att gat gca 307
 Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu Leu Ala Ile Asp Ala
 55 60 65
 tcg gat atg gtc aga ctc gtt gac tca ctt gag gta cgc ggc tgg gcg 355
 Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu Val Arg Gly Trp Ala
 70 75 80 85
 aaa agg gaa cgt gat ccc aaa gac cgt cgt cgc caa att gtt gcg tca 403
 Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg Gln Ile Val Ala Ser
 90 95 100
 acg aag aag gga aaa aac gcc cag gcg gat ctg cac aaa gtt gtg ctt 451

Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu His Lys Val Val Leu
 105 110 115

gag gca gag gat gct gcg ttg gat gag tct acg tcc aag cag ttg aag 499
 Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr Ser Lys Gln Leu Lys
 120 125 130

cac ctt cgt aaa ttg gcc gca gca att atc tcc acc gaa gag gac 544
 His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser Thr Glu Glu Asp
 135 140 145

taaataaac gtggcattga gca 567

<210> 90
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 90
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 20 25 30

Glu Leu Ala Lys His Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr
 35 40 45

Cys Leu Val His Ser Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu
 50 55 60

Leu Ala Ile Asp Ala Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu
 65 70 75 80

Val Arg Gly Trp Ala Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg
 85 90 95

Gln Ile Val Ala Ser Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu
 100 105 110

His Lys Val Val Leu Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr
 115 120 125

Ser Lys Gln Leu Lys His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser
 130 135 140

Thr Glu Glu Asp
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<210> 91
 <211> 272
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (37)..(249)
 <223> RXA01125

<400> 91

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                                   Met Ala Ile Ile Val Asp
                                   1                               5

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Ile Asp Val Met Leu Ala Arg Arg Lys Met Gly Val Gly Glu Leu Ala
              10                      15                      20

gaa aaa atc ggc atc acc cca gcc aac ctc tcg gtc tta aaa aac ggg 150
Glu Lys Ile Gly Ile Thr Pro Ala Asn Leu Ser Val Leu Lys Asn Gly
              25                      30                      35

cgc gca aaa gcg ata cgc ttc agc aca ttg gag gcc att tgc cgc gag 198
Arg Ala Lys Ala Ile Arg Phe Ser Thr Leu Glu Ala Ile Cys Arg Glu
              40                      45                      50

ctc ggc tgc cag ccg ggc gac att ttg cgt tac gac gcc tcc ctc cac 246
Leu Gly Cys Gln Pro Gly Asp Ile Leu Arg Tyr Asp Ala Ser Leu His
              55                      60                      65                      70

aac taaacccgaa acgcaaagag ccc 272
Asn

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<210> 92

<211> 71

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 92

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Gly Val Gly Glu Leu Ala Glu Lys Ile Gly Ile Thr Pro Ala Asn Leu
              20              25              30

Ser Val Leu Lys Asn Gly Arg Ala Lys Ala Ile Arg Phe Ser Thr Leu
              35              40              45

Glu Ala Ile Cys Arg Glu Leu Gly Cys Gln Pro Gly Asp Ile Leu Arg
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Tyr Asp Ala Ser Leu His Asn
 65              70

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<210> 93

<211> 804

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(781)

<223> RXN00822

<400> 93

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cggactcaaa caagatgtgt gcagatgaag gagaaaagca	gtg gaa ggt gta cag	115
	Val Glu Gly Val Gln	
	1 5	
gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca	163	
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala		
	10 15 20	
gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga	211	
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly		
	25 30 35	
gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc	259	
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile		
	40 45 50	
acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa	307	
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu		
	55 60 65	
aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc	355	
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser		
	70 75 80 85	
atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa	403	
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu		
	90 95 100	
gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct	451	
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala		
	105 110 115	
gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt	499	
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg		
	120 125 130	
ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc	547	
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val		
	135 140 145	
cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc	595	
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly		
	150 155 160 165	
acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctc act cag gaa	643	
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu		
	170 175 180	
gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct	691	
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala		
	185 190 195	
ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc	739	
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser		
	200 205 210	
gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga	781	
Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg		
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taatcaccaa agcgcataaaa agc	804	

<210> 94
<211> 227
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
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20 25 30
Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp
35 40 45
Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala
50 55 60
Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met
65 70 75 80
Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala
85 90 95
Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu
100 105 110
Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg
115 120 125
Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu
130 135 140
Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu
145 150 155 160
Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His
165 170 175
Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu
180 185 190
Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg
195 200 205
Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg
210 215 220
Arg Ala Arg
225

<210> 95
<211> 804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(781)

<223> FRXA00822

<400> 95

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cggactcaaa caagatgtgt gcagatgaag gagaaaagca gtg gaa ggt gta cag 115
Val Glu Gly Val Gln
1 5

gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca 163
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala
10 15 20

gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga 211
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly
25 30 35

gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc 259
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile
40 45 50

acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa 307
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu
55 60 65

aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc 355
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser
70 75 80 85

atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa 403
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu
90 95 100

gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct 451
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala
105 110 115

gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt 499
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg
120 125 130

ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc 547
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val
135 140 145

cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc 595
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly
150 155 160 165

acc caa gaa gct ggc gcg ctg cgc gtg aac cac gac ctc act cag gaa 643
Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu
170 175 180

gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct 691
Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala
185 190 195

ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc 739
Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser
200 205 210

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gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga 781
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<210> 96

<211> 227

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

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Val Asp Pro Thr Ala Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val
 20 25 30

Arg Phe Pro Arg Gly Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp
 35 40 45

Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala
 50 55 60

Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met
 65 70 75 80

Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala
 85 90 95

Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu
 100 105 110

Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg
 115 120 125

Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu
 130 135 140

Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu
 145 150 155 160

Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His
 165 170 175

Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu
 180 185 190

Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg
 195 200 205

Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg
 210 215 220

Arg Ala Arg
 225

<210> 97

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<220>
<221> CDS
<222> (101)..(421)
<223> RXN00849
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<210> 98
<211> 107
<212> PRT
<213> Corynebacterium glutamicum
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Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
20 25 30
Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
35 40 45
Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly

<210>	100
<211>	107
<212>	PRT

<213> Corynebacterium glutamicum

<400> 100

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Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
 1              5              10              15

Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
          20              25              30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
          35              40              45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
 50              55              60

Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
 65              70              75              80

Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
          85              90              95

Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
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<210> 101

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXA02698

<400> 101

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aagattctcc attagagctc gaaccagcta aattaagact gtg agt tcc aac aat 115
                                         Val Ser Ser Asn Asn
                                         1              5

gaa tct tcc ttc gcc ctg ccc gac aat gaa cca ttg ctg acc ctt ccg 163
Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro Leu Leu Thr Leu Pro
          10              15              20

gag aca gcc gag cgc ctc ggc gtt gtt gtc acc aag gtg atg gat ctg 211
Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr Lys Val Met Asp Leu
          25              30              35

gtc aat gaa cac aaa ttg atc gtg gtc cgg cgc gac ggt att cgc tac 259
Val Asn Glu His Lys Leu Ile Val Val Arg Arg Asp Gly Ile Arg Tyr
          40              45              50

att cca gaa gct ttc ctg agc acc aag aag gaa aac acc aac cgt ttc 307
Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu Asn Thr Asn Arg Phe
          55              60              65

atc cct gga gtt att gcc ttg ctt gcc gac ggt ggc ttc agc gac gag 355
Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly Gly Phe Ser Asp Glu
          70              75              80              85

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<400> 103
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gaatatcggg tcgatcgctt ttaaacactc aggaggatcc ttg ccg gcc aaa atc    115
                                   Leu Pro Ala Lys Ile
                                   1       5

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acg gac act cgt ccc acc cca gaa tcc ctt cac gct gtt gaa gag gaa 163
 Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His Ala Val Glu Glu Glu
 10 15 20

acc gca gcc ggt gcc cgc agg att gtt gcc acc tat tct aag gac ttc 211
 Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr Tyr Ser Lys Asp Phe
 25 30 35

ttc gac ggc gtc act ttg atg tgc atg ctc ggc gtt gaa cct cag ggc 259
 Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly Val Glu Pro Gln Gly
 40 45 50

ctg cgt tac acc aag gtc gct tct gaa cac gag gaa gct cag cca aag 307
 Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu Glu Ala Gln Pro Lys
 55 60 65

aag gct aca aag cgg act cgt aag gca cca gct aag aag gct gct gct 355
 Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala Lys Lys Ala Ala Ala
 70 75 80 85

aag aaa acg acc aag aag acc act aag aaa act act aaa aag acc acc 403
 Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr
 90 95 100

gca aag aag acc aca aag aag tct taagccggat cttatatgga tga 450
 Ala Lys Lys Thr Thr Lys Lys Ser
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<210> 104

<211> 109

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 104

Leu Pro Ala Lys Ile Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His
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 20 25 30

Tyr Ser Lys Asp Phe Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly
 35 40 45

Val Glu Pro Gln Gly Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu
 50 55 60

Glu Ala Gln Pro Lys Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala
 65 70 75 80

Lys Lys Ala Ala Ala Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr
 85 90 95

Thr Lys Lys Thr Thr Ala Lys Lys Thr Thr Lys Lys Ser
 100 105

<210> 105

<211> 495

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(495)

<223> RXA02830

<400> 105

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Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly
  1             5             10             15

ctg gcg ctg aca ggg gcg ggc gat cag ctt ttg tcg cag gcg cgc cgc      96
Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg
             20             25             30

ctg atc gcc ctg aac gac gag gta tac gcc cgc ttg aac gcc ggt gcc     144
Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala
             35             40             45

tac gag ggc gag gtg acg ctg ggc gtg cct caa gac gtg atc tac ccc     192
Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro
             50             55             60

gtc atc ccg cgc gtc ttg cag caa ttc gcc cgc gat ttt ccc cgc gtg     240
Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val
             65             70             75             80

caa att cac ctg atc tcg aac ttc acg ctg atg ctg aaa gaa cag ttc     288
Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe
             85             90             95

cgc cgc ggc gaa atc gac gtg atg ctg acg acc gag gac gag ctg ggc     336
Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly
             100            105            110

gag ggc ggc gag acg ctg gcc cag cgc gag ctg atc tgg gtc ggc gca     384
Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala
             115            120            125

ccg ggc ggg tcg gcg tgg acc cgc agg ccg ctg ccc ttg gcg ttt gaa     432
Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu
             130            135            140

cgc gcc tgc att ttc cgg tct ttc ttg cag cgc cgc ttg gat gcc aac     480
Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn
             145            150            155            160

agc atc tat tgg caa
Ser Ile Tyr Trp Gln
             165

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<210> 106

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly
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 20 25 30
 Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala
 35 40 45
 Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro
 50 55 60
 Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val
 65 70 75 80
 Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe
 85 90 95
 Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly
 100 105 110
 Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala
 115 120 125
 Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu
 130 135 140
 Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn
 145 150 155 160
 Ser Ile Tyr Trp Gln
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<210> 107
 <211> 459
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(436)
 <223> RXA00947

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 taaattcaat actgttttac gagatcattt ggaggggtgtc atg gcc cgc aaa ttg 115
 Met Ala Arg Lys Leu
 1 5
 gaa cat cca tct ttg gcc gag atg aat tta aat gcc atc atg ttt gcg 163
 Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn Ala Ile Met Phe Ala
 10 15 20
 ctg tcg gat cct att agg cga caa atc ctg tcg cag ctg tcg tgc gga 211
 Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser Gln Leu Ser Cys Gly
 25 30 35
 cat aat gat cag gca tgt gtt gcc ttc gag ctt cca gta tct aaa tcc 259
 His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu Pro Val Ser Lys Ser
 40 45 50

acc tca acg cac cac ttc cgc gta ctc cgt gag gcg ggt ctg att act 307
 Thr Ser Thr His His Phe Arg Val Leu Arg Glu Ala Gly Leu Ile Thr
 55 60 65

cag cgc tat gaa gga act gcc att cta agt gcg ctg cgc agc gaa gat 355
 Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala Leu Arg Ser Glu Asp
 70 75 80 85

atg gaa gcg cgt ttt ccg gga ctg ctg act tct gtc atg cga gcg gaa 403
 Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser Val Met Arg Ala Glu
 90 95 100

gtg gaa gag cgc aac gca gct gac ttg ccc gtt taggacgggt agcaagtatt 456
 Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
 105 110

atc 459

<210> 108
 <211> 112
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
 Met Ala Arg Lys Leu Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn
 1 5 10 15

Ala Ile Met Phe Ala Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser
 20 25 30

Gln Leu Ser Cys Gly His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu
 35 40 45

Pro Val Ser Lys Ser Thr Ser Thr His His Phe Arg Val Leu Arg Glu
 50 55 60

Ala Gly Leu Ile Thr Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala
 65 70 75 80

Leu Arg Ser Glu Asp Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser
 85 90 95

Val Met Arg Ala Glu Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
 100 105 110

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA01836

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	Met	Gly	Gln	Gln	Glu	
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att atc gag gac tcc acc gag agc ggt att aag gtt tta gac cgc act						163
Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys Val Leu Asp Arg Thr						
	10				20	
gta tta atc ctc aat gtc atc gca gaa cag cct cga tcg ttg gca gag						211
Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro Arg Ser Leu Ala Glu						
	25				35	
ctc gca gct gcc acc gat ctg ccc agg gct aca gcc cac cgc ctc gcc						259
Leu Ala Ala Ala Thr Asp Leu Pro Arg Ala Thr Ala His Arg Leu Ala						
	40				50	
tca gcg ctt gag gta cac ggc atg ttg gca cgc tcc cgc gat aat aga						307
Ser Ala Leu Glu Val His Gly Met Leu Ala Arg Ser Arg Asp Asn Arg						
	55				65	
tgg acc atc ggc gca cgg ctt gcc tca ttg ggt gca cgc ggc gct gac						355
Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly Ala Arg Gly Ala Asp						
	70				85	
acc ctc atc gat acg gcc gta cca att atg gcc gac ctt atg gag cgc						403
Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala Asp Leu Met Glu Arg						
	90				100	
acc ggc gaa tcc gtt cag ctt tat cgc ctc acc ggc acc acc cgc acg						451
Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr Gly Thr Thr Arg Thr						
	105				115	
tgt gtg gcc agc caa gag ccc agc tcc ggg cta aaa aac gtg gtt ccc						499
Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu Lys Asn Val Val Pro						
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Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser Ala Ala Arg Val Phe						
	135				145	
gcc gcc tac ctc ccc atc ccc tct gcc agc gtc ttt tcc cgc gag gag						595
Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val Phe Ser Arg Glu Glu						
	150				165	
ctt gac cag gtg cgc gcc agc ggc tta gcg gag tcc gtg ggc gag cgt						643
Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu Ser Val Gly Glu Arg						
	170				180	
gag ctc ggc ctt gct agc ctc tcc tcc cct gtt ttt gat tcc aac gga						691
Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val Phe Asp Ser Asn Gly						
	185				195	
tcc atg atc gcg gca ctg tcc atc tcc ggc gtg gcc gag cgc ctc aag						739
Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val Ala Glu Arg Leu Lys						
	200				210	
ccc cac ccc gcc gcc atg tgg ggc acc gag ctt atc gac gcc gcc gag						787
Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu Ile Asp Ala Ala Glu						
	215				225	
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Arg Leu Gly Ala Leu Leu						

230

235

<210> 110

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

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Arg Ser Leu Ala Glu Leu Ala Ala Thr Asp Leu Pro Arg Ala Thr
 35 40 45

Ala His Arg Leu Ala Ser Ala Leu Glu Val His Gly Met Leu Ala Arg
 50 55 60

Ser Arg Asp Asn Arg Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly
 65 70 75 80

Ala Arg Gly Ala Asp Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala
 85 90 95

Asp Leu Met Glu Arg Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr
 100 105 110

Gly Thr Thr Arg Thr Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu
 115 120 125

Lys Asn Val Val Pro Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser
 130 135 140

Ala Ala Arg Val Phe Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val
 145 150 155 160

Phe Ser Arg Glu Glu Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu
 165 170 175

Ser Val Gly Glu Arg Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val
 180 185 190

Phe Asp Ser Asn Gly Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val
 195 200 205

Ala Glu Arg Leu Lys Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu
 210 215 220

Ile Asp Ala Ala Glu Arg Leu Gly Ala Leu Leu
 225 230 235

<210> 111

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(754)

<223> RXA00292

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                                         Met Asp Gln Thr Leu
                                         1 5

aaa gtt tta gta att gat gat gat ttc cgc gtc gcc ggc att cac gcc 163
Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val Ala Gly Ile His Ala
                        10 15 20

tcc atc gtt gat gcg tcc cct gga ttt tcg gtg gtc ggt acc gcg cgt 211
Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val Val Gly Thr Ala Arg
                        25 30 35

acc ctc gca gag gca aaa acc ctg atc gcc aca ttt tcc ccg gat ctc 259
Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr Phe Ser Pro Asp Leu
                        40 45 50

cta ctt gtt gat gtc tac ctc ccc gac ggc gat ggc att gac ctc gtg 307
Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp Gly Ile Asp Leu Val
                        55 60 65

ggc acc tcc aat att gat gcg ttt gtg ctc agc gca gcc gat gac atc 355
Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser Ala Ala Asp Asp Ile
                        70 75 80 85

aaa aca gtt cga cgc gcc atg cgt gcc ggg gca ctc gga tat ctg ctc 403
Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala Leu Gly Tyr Leu Leu
                        90 95 100

aaa cca ttt ccc caa aaa cgt ctc gtg gaa cgc ctt gac cgt tac gtc 451
Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg Leu Asp Arg Tyr Val
                        105 110 115

cgc tac cgc cat gtc tta tcc ggc acc caa gga ctt tcc caa gac aaa 499
Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly Leu Ser Gln Asp Lys
                        120 125 130

att gac cag gca acc gca atc ctc aac ggc acc caa gcg ccg gtc acc 547
Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr Gln Ala Pro Val Thr
                        135 140 145

gtc tct aga tcc gcc aca gag caa tta ctt ctc gac gcc ctg gaa ggc 595
Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu Asp Ala Leu Glu Gly
                        150 155 160 165

caa gaa ctc tcc gca aca gaa gct tcc gaa gct gcc gga gtt tca cgt 643
Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala Ala Gly Val Ser Arg
                        170 175 180

gcc aca gca cag cgc agg ctg gca gcg atg gct agc caa ggt gtg atc 691
Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala Ser Gln Gly Val Ile
                        185 190 195

cag gtt cgc ctt cgg tac gga cag tcc ggg cga cca gaa cat cta tat 739
Gln Val Arg Leu Arg Tyr Gly Gln Ser Gly Arg Pro Glu His Leu Tyr

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<210> 112
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<212> PRT
<213> Corynebacterium glutamicum

<400> 112
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20 25 30
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35 40 45
Phe Ser Pro Asp Leu Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp
50 55 60
Gly Ile Asp Leu Val Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser
65 70 75 80
Ala Ala Asp Asp Ile Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala
85 90 95
Leu Gly Tyr Leu Leu Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg
100 105 110
Leu Asp Arg Tyr Val Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly
115 120 125
Leu Ser Gln Asp Lys Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr
130 135 140
Gln Ala Pro Val Thr Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu
145 150 155 160
Asp Ala Leu Glu Gly Gln Glu Leu Ser Ala Thr Glu Ala Ser Glu Ala
165 170 175
Ala Gly Val Ser Arg Ala Thr Ala Gln Arg Arg Leu Ala Ala Met Ala
180 185 190
Ser Gln Gly Val Ile Gln Val Arg Leu Arg Tyr Gly Gln Ser Gly Arg
195 200 205
Pro Glu His Leu Tyr Ser Lys Pro Leu Leu
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<210> 113
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<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3202)

<223> RXA00182

<400> 113

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gttacgagaa accactcttc aacataggtg aaatgaattc atg act tct cac ttg 115
                                         Met Thr Ser His Leu
                                         1 5

ctt cac ggt ctc tgg atc aaa gat cgc ggt ctg caa ctg tgg att gag 163
Leu His Gly Leu Trp Ile Lys Asp Arg Gly Leu Gln Leu Trp Ile Glu
                        10 15 20

cag gtc gaa ggg cac cga att gtg ctt cca gag gcg gtg gaa aaa ggc 211
Gln Val Glu Gly His Arg Ile Val Leu Pro Glu Ala Val Glu Lys Gly
                        25 30 35

acg ttc ccg ccg gta gtg gag caa atc ctc gac ggg aaa acc ttc cgc 259
Thr Phe Pro Pro Val Val Glu Gln Ile Leu Asp Gly Lys Thr Phe Arg
                        40 45 50

gcg cgc atg aat gtg cat ctg cgc act ccg aaa ggg cgc cat gtt gag 307
Ala Arg Met Asn Val His Leu Arg Thr Pro Lys Gly Arg His Val Glu
                        55 60 65

ctg ccc acg cca aca gca gct ttt acc cct gaa gaa gca gtc acg gtt 355
Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu Glu Ala Val Thr Val
                        70 75 80 85

ttc tca caa tta agt ttt ttg aaa gca gaa acc cct gcc gcc acc cga 403
Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr Pro Ala Ala Thr Arg
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gcg caa cgt gac tcc att gcg ccc gat ctg tgg tgg ctg att gtc atg 451
Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp Trp Leu Ile Val Met
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tat caa ggc ctg gcg cgt ttt gtg cag gcc ggc cgc gtc acg ctt cgc 499
Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly Arg Val Thr Leu Arg
                        120 125 130

acg gtg atg atg gat aat gcc tgg tgg ccc cag tgg caa cta tct gcc 547
Thr Val Met Met Asp Asn Ala Trp Trp Pro Gln Trp Gln Leu Ser Ala
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agc ctg tcg gag cgt ggg tgg ctc gcg gaa atg aac cat gcc gcg ccg 595
Ser Leu Ser Glu Arg Gly Trp Leu Ala Glu Met Asn His Ala Ala Pro
                        150 155 160 165

ggt att ttg ccg att aat ggt ggc cga gat ttg gcc gga agc atg tcc 643
Gly Ile Leu Arg Ile Asn Gly Gly Arg Asp Leu Ala Gly Ser Met Ser
                        170 175 180

aat gag ctt ccg cac tgg atc gcc aac gcc att ttg cgt gat tac cgc 691
Asn Glu Leu Pro His Trp Ile Ala Asn Ala Ile Leu Arg Asp Tyr Arg
                        185 190 195

gat gaa acc atg ccg tat gcg cgc cat gag ttt gtt gag gcg ttg ctg 739

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Asp	Glu	Thr	Met	Pro	Tyr	Ala	Arg	His	Glu	Phe	Val	Glu	Ala	Leu	Leu		
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Phe	Asn	His	Ser	Leu	Arg	Lys	Gly	Ser	Thr	Met	Leu	Thr	His	Ala	Leu		
	215					220					225						
aat	cag	tgg	aaa	aac	acc	att	aca	tct	gcg	tct	ttg	cag	ctg	gtg	att	835	
Asn	Gln	Trp	Lys	Asn	Thr	Ile	Thr	Ser	Ala	Ser	Leu	Gln	Leu	Val	Ile		
230					235					240					245		
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Leu	Val	Glu	Glu	Pro	Pro	Ala	Glu	Ser	Asp	Tyr	Glu	Asp	Pro	Met	Asp		
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Ser	Val	Trp	Pro	Val	Arg	Leu	Met	Val	Arg	Thr	Gly	Val	Asp	Ala	Pro		
			265					270					275				
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Gln	Ala	Ile	Gln	Lys	Gly	Ser	Ile	Asp	Ser	Gly	Gly	Met	Glu	Gln	Leu		
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310					315					320					325		
ggg	gac	tgg	gat	att	ttc	tta	acc	acc	gag	gag	atc	gtc	aac	ttt	atc	1123	
Gly	Asp	Trp	Asp	Ile	Phe	Leu	Thr	Thr	Glu	Glu	Ile	Val	Asn	Phe	Ile		
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tcc	cac	gat	gta	gcc	aag	ctg	cgc	aaa	gcc	ggc	att	ccc	gtc	atg	ctg	1171	
Ser	His	Asp	Val	Ala	Lys	Leu	Arg	Lys	Ala	Gly	Ile	Pro	Val	Met	Leu		
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ccc	aaa	gcc	tgg	agc	acc	tat	gaa	acc	cgc	gcg	cag	gtg	gaa	gcg	cgc	1219	
Pro	Lys	Ala	Trp	Ser	Thr	Tyr	Glu	Thr	Arg	Ala	Gln	Val	Glu	Ala	Arg		
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Thr	Pro	Asn	Asp	Ala	Ala	Asp	Ser	Ser	Thr	Lys	Ala	Ile	Ile	Gly	Leu		
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gac	cag	ctc	gtg	gaa	tac	aac	tgg	cgc	atc	agc	gtc	ggc	gat	att	cag	1315	
Asp	Gln	Leu	Val	Glu	Tyr	Asn	Trp	Arg	Ile	Ser	Val	Gly	Asp	Ile	Gln		
390					395					400					405		
ctg	tcc	gac	gaa	gag	atg	cgc	gaa	ctc	atc	gat	tcc	aaa	aca	ggc	ctc	1363	
Leu	Ser	Asp	Glu	Glu	Met	Arg	Glu	Leu	Ile	Asp	Ser	Lys	Thr	Gly	Leu		
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atc	cgc	ctg	cgc	ggc	gat	tgg	gtc	atg	gcg	gac	caa	gac	gcg	ttg	cga	1411	
Ile	Arg	Leu	Arg	Gly	Asp	Trp	Val	Met	Ala	Asp	Gln	Asp	Ala	Leu	Arg		
			425					430					435				
cgc	atc	acc	agc	tac	atg	gag	gaa	cta	tca	aag	tcc	tcc	gaa	aaa	cgc	1459	
Arg	Ile	Thr	Ser	Tyr	Met	Glu	Glu	Leu	Ser	Lys	Ser	Ser	Glu	Lys	Arg		

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gca aac ggc gaa gaa ggt Ala Asn Gly Glu Glu Gly 470	tgg caa ctc ctg gct Trp Gln Leu Leu Ala 475	gcc aag gct gaa act Ala Ala Lys Ala Glu Thr 480	1555
ctc cgc aag gaa ttc aat Leu Arg Lys Glu Phe Asn 490	gag aaa ttc agt ggc Glu Lys Phe Ser Gly 495	gat gga caa ggc gaa Asp Gly Gln Gly Glu 500	1603
gta acc ctt gct gaa ctg Val Thr Leu Ala Glu Leu 505	cgc gaa atc gca ctg Arg Glu Ile Ala Leu 510	aaa gcc gcc gaa aac Lys Ala Ala Glu Asn 515	1651
gaa cca gtg gaa ttc acc Glu Pro Val Glu Phe Thr 520	ggc tcg caa tgg ttc Gly Ser Gln Trp Phe 525	aac tcc ttg ctc ggc Asn Ser Leu Leu Gly 530	1699
ggc acc gaa aca ccc gcg Gly Thr Glu Thr Pro Ala 535	ccg gtg cgc gtc gac Pro Val Arg Val Asp 540	atc ccc gac acg gtc Ile Pro Asp Thr Val 545	1747
ctt gct gac ctg cgc gaa Leu Ala Asp Leu Arg Glu 550	tac cag cga cgc ggc Tyr Gln Arg Arg Gly 555	gtg gac tgg ctg tac Val Asp Trp Leu Tyr 560	1795
tgg atg tcc gca aat aat Trp Met Ser Ala Asn Asn 570	tta ggt gca gtg ctt Leu Gly Ala Val Leu 575	gcc gac gac atg ggc Ala Asp Asp Met Gly 580	1843
ttg gga aaa acc ctc cag Leu Gly Lys Thr Leu Gln 585	ttg ttc tcc ctt ttg Leu Leu Ser Leu Leu 590	gca gtc gag cgc gca Ala Val Glu Arg Ala 595	1891
gaa aac cca gag ttg gaa Glu Asn Pro Glu Leu Glu 600	cgc ggc ccg acg ctc Arg Gly Pro Thr Leu 605	gtg gtg tgc cca aca Val Val Cys Pro Thr 610	1939
tct gtg gtg gga aac tgg Ser Val Val Gly Asn Trp 615	gca gcc gag gcg gct Ala Ala Glu Ala Ala 620	aaa ttt gtg cct tca Lys Phe Val Pro Ser 625	1987
cta aag gta ttg atg cat Leu Lys Val Leu Met His 630	cac ggc ccg cag cgt His Gly Pro Gln Arg 635	ttg aat gat gcc gat Leu Asn Asp Ala Asp 640	2035
ttc ctg agt caa tcc aag Phe Leu Ser Gln Ser Lys 650	ggc atg gac ttg att Gly Met Asp Leu Ile 655	atc acc tca tac ggt Ile Ile Thr Ser Tyr Gly 660	2083
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Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His Arg Val Ala Leu Thr	
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Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met Arg Ser Ile Leu Asp	
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Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser Phe Phe Arg Asn His	
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Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp Thr Met Thr Glu Arg	
745 750 755	
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Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg Arg Leu Lys Thr Asp	
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ccg aat atc atc gac gat ctg cct gag aaa acc gaa cag atc atc cgc	2467
Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr Glu Gln Ile Ile Arg	
775 780 785	
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Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr Lys Ala Leu Val Glu	
790 795 800 805	
gat gtg cag aaa caa ctc gat gaa cgc caa gga atg tca cgt aaa ggc	2563
Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly Met Ser Arg Lys Gly	
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Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln Ile Cys Asn His Pro	
825 830 835	
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Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr Leu Lys Gly Lys His	
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cgt tcc ggc aag gtg gaa gcg ctc atg gaa ctg atc gat acg gca gta	2707
Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu Ile Asp Thr Ala Val	
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aaa gaa gag cgc cgc atg ctg atc ttc acc cag tac gca gcc ttt ggc	2755
Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln Tyr Ala Ala Phe Gly	
870 875 880 885	
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Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu Gly Thr Asn Ile Pro	
890 895 900	
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Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg Asp Arg Met Val Ala	
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920 925 930	

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 950 955 960 965

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 Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp Ile Leu Asp Gly Lys
 985 990 995

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 35 40 45

Gly Lys Thr Phe Arg Ala Arg Met Asn Val His Leu Arg Thr Pro Lys
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Gly Arg His Val Glu Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu
 65 70 75 80

Glu Ala Val Thr Val Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr
 85 90 95

Pro Ala Ala Thr Arg Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp
 100 105 110

Trp Leu Ile Val Met Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly
 115 120 125

Arg Val Thr Leu Arg Thr Val Met Met Asp Asn Ala Trp Trp Pro Gln
 130 135 140

Trp	Gln	Leu	Ser	Ala	Ser	Leu	Ser	Glu	Arg	Gly	Trp	Leu	Ala	Glu	Met	145	150	155	160
Asn	His	Ala	Ala	Pro	Gly	Ile	Leu	Arg	Ile	Asn	Gly	Gly	Arg	Asp	Leu	165	170		175
Ala	Gly	Ser	Met	Ser	Asn	Glu	Leu	Pro	His	Trp	Ile	Ala	Asn	Ala	Ile	180	185		190
Leu	Arg	Asp	Tyr	Arg	Asp	Glu	Thr	Met	Pro	Tyr	Ala	Arg	His	Glu	Phe	195	200		205
Val	Glu	Ala	Leu	Leu	Phe	Asn	His	Ser	Leu	Arg	Lys	Gly	Ser	Thr	Met	210	215		220
Leu	Thr	His	Ala	Leu	Asn	Gln	Trp	Lys	Asn	Thr	Ile	Thr	Ser	Ala	Ser	225	230		235
Leu	Gln	Leu	Val	Ile	Leu	Val	Glu	Glu	Pro	Pro	Ala	Glu	Ser	Asp	Tyr	245	250		255
Glu	Asp	Pro	Met	Asp	Ser	Val	Trp	Pro	Val	Arg	Leu	Met	Val	Arg	Thr	260	265		270
Gly	Val	Asp	Ala	Pro	Gln	Ala	Ile	Gln	Lys	Gly	Ser	Ile	Asp	Ser	Gly	275	280		285
Gly	Met	Glu	Gln	Leu	Arg	Ser	Gln	Tyr	Glu	Thr	Ala	Lys	Thr	Thr	Ser	290	295		300
Met	Leu	Leu	Asp	Pro	Ala	Arg	Glu	Asp	Ala	Met	Leu	Gly	His	Met	Val	305	310		315
Asp	Ile	Ala	Gln	Asn	Gly	Asp	Trp	Asp	Ile	Phe	Leu	Thr	Thr	Glu	Glu	325	330		335
Ile	Val	Asn	Phe	Ile	Ser	His	Asp	Val	Ala	Lys	Leu	Arg	Lys	Ala	Gly	340	345		350
Ile	Pro	Val	Met	Leu	Pro	Lys	Ala	Trp	Ser	Thr	Tyr	Glu	Thr	Arg	Ala	355	360		365
Gln	Val	Glu	Ala	Arg	Thr	Pro	Asn	Asp	Ala	Ala	Asp	Ser	Ser	Thr	Lys	370	375		380
Ala	Ile	Ile	Gly	Leu	Asp	Gln	Leu	Val	Glu	Tyr	Asn	Trp	Arg	Ile	Ser	385	390		395
Val	Gly	Asp	Ile	Gln	Leu	Ser	Asp	Glu	Glu	Met	Arg	Glu	Leu	Ile	Asp	405	410		415
Ser	Lys	Thr	Gly	Leu	Ile	Arg	Leu	Arg	Gly	Asp	Trp	Val	Met	Ala	Asp	420	425		430
Gln	Asp	Ala	Leu	Arg	Arg	Ile	Thr	Ser	Tyr	Met	Glu	Glu	Leu	Ser	Lys	435	440		445
Ser	Ser	Glu	Lys	Arg	Ala	Arg	Thr	Glu	Met	Glu	Lys	Val	Ala	Met	Gln	450	455		460

Ala Lys Leu Ala Glu Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala
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 Ala Lys Ala Glu Thr Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly
 485 490 495
 Asp Gly Gln Gly Glu Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu
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 Lys Ala Ala Glu Asn Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe
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 Asn Ser Leu Leu Gly Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp
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 Ile Pro Asp Thr Val Leu Ala Asp Leu Arg Glu Tyr Gln Arg Arg Gly
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 Ala Val Glu Arg Ala Glu Asn Pro Glu Leu Glu Arg Gly Pro Thr Leu
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 Val Val Cys Pro Thr Ser Val Val Gly Asn Trp Ala Ala Glu Ala Ala
 610 615 620
 Lys Phe Val Pro Ser Leu Lys Val Leu Met His His Gly Pro Gln Arg
 625 630 635 640
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 645 650 655
 Ile Thr Ser Tyr Gly Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln
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 Val Gly Phe Glu Arg Val Val Leu Asp Glu Ala Gln Ala Ile Lys Asn
 675 680 685
 Ser Ser Thr Arg Val Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His
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 Thr Met Thr Glu Arg Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg
 755 760 765
 Arg Leu Lys Thr Asp Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr
 770 775 780
 Glu Gln Ile Ile Arg Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr

785 790 795 800
 Lys Ala Leu Val Glu Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly
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 850 855 860
 Ile Asp Thr Ala Val Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln
 865 870 875 880
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 Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp
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 Val Tyr Lys Met Ile Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp
 980 985 990
 Ile Leu Asp Gly Lys Thr His Leu Ala Ser Ala Ile Val Gly Glu Gly
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Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn Phe Gly Ala Ser Phe	
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Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala Glu Ala Asp Val Glu	
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Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro	
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Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp	
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Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys Phe Thr Arg Glu Leu	
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Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln Cys Tyr Ser Gly Tyr	
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Val Glu Asp Asp Ile Phe Glu Val Val Val Pro Ile Glu Gln Val Thr	
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Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys Arg Lys Leu Leu Pro	
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Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp Arg Val Trp Ser Val	
185 190 195	
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Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val Gly Asn Glu Gly Asn	
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Ala Thr Pro Val Lys His Arg Asp Val Ala Lys Phe Leu Met Pro Gln	
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 Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln
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 Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg
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<212> DNA

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Ala	Asn	Leu	Val	Glu	Ser	Gly	Gly	Ala	Ala	Lys	Asp	Ala	Ile	Ala	Asn	
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Gly	Asp	Val	Thr	Val	Asn	Gly	Glu	Val	Asp	Thr	Arg	Arg	Gly	Lys	Thr	
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Arg Arg Gly Lys Thr Leu Arg Asp Gly Asp Val Val Cys Ile Gly Glu
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Met

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 Met Ser Gln Lys Ile
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 Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu Met Leu Thr Ile Val
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Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp Leu Ile Leu Leu Asp
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Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile Cys Arg Leu Ile Arg
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caa gaa tcc tcc gta ccc atc atc atg ctc acc gcc aaa acc gac acc 355
Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr Ala Lys Thr Asp Thr
      70                      75                      80                      85

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Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala Asp Asp Tyr Val Asn
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Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg Ile Arg Ala Arg Leu
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cgc gca acc gtg gac gag ccc agc gaa atc atc gaa gtc ggc gat ctg 499
Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile Glu Val Gly Asp Leu
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Ser Ile Asp Val Pro Ala His Thr Val Lys Arg Asn Gly Ala Glu Ile
      135                      140                      145

tcc ttg acc cca ctc gaa ttc gac ctc ctg ctg gaa ctc gcc cgc aaa 595
Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu Glu Leu Ala Arg Lys
      150                      155                      160                      165

cca cag caa gta ttc acc cgt gaa gaa ttg ctg ggc aaa gtg tgg ggc 643
Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu Gly Lys Val Trp Gly
      170                      175                      180

tac cgc cac gca tcc gac act cga ctg gtc aac gtt cac gtt cag cgt 691
Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn Val His Val Gln Arg
      185                      190                      195

ctg cgc gcc aag att gaa aaa gat cca gaa aat ccg cag atc gtc ctc 739
Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn Pro Gln Ile Val Leu
      200                      205                      210

acc gtc cgc ggt gtt ggc tac aaa act ggc cac aac gat taagtttttc 788
Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His Asn Asp
      215                      220                      225

atttaaaaaa ggg 801

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<210> 120

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Met Ser Gln Lys Ile Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu
 1 5 10 15

Met Leu Thr Ile Val Leu Ser Ala Glu Gly Phe Asp Thr Val Ala Val
 20 25 30

Thr Asp Gly Ala Leu Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp
 35 40 45

Leu Ile Leu Leu Asp Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile
 50 55 60

Cys Arg Leu Ile Arg Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr
 65 70 75 80

Ala Lys Thr Asp Thr Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala
 85 90 95

Asp Asp Tyr Val Asn Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg
 100 105 110

Ile Arg Ala Arg Leu Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile
 115 120 125

Glu Val Gly Asp Leu Ser Ile Asp Val Pro Ala His Thr Val Lys Arg
 130 135 140

Asn Gly Ala Glu Ile Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu
 145 150 155 160

Glu Leu Ala Arg Lys Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu
 165 170 175

Gly Lys Val Trp Gly Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn
 180 185 190

Val His Val Gln Arg Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn
 195 200 205

Pro Gln Ile Val Leu Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His
 210 215 220

Asn Asp
 225

<210> 121

<211> 1149

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1126)

<223> RXA00885

<400> 121

caacctggcg gtagccgatg cgggacgttt gcttgccgac ggcatcatcg cgcacatttt 60

gcttagtgaa gaagactaaa tatttagtag gggtacagac atg gtg agt gca aca 115

	Met	Val	Ser	Ala	Thr	
	1				5	
gag aaa cgt aga tac gaa gtg ttg cgg gcc atc gtc gct gat tac att						163
Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile Val Ala Asp Tyr Ile						
				10		
					20	
gcg tct cag gaa cct gtc gga tgc aag tca ctc ctc gag cgc cat aag						211
Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu Leu Glu Arg His Lys						
				25		
					35	
ctc aac gtg agt tct gcg acg atc cgc aac gat atg tgc gtg ctg gaa						259
Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp Met Ser Val Leu Glu						
				40		
					50	
tcc gat ggc ttt atc gtc cag gag cat gca agt tct ggc cgg gta cca						307
Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser Ser Gly Arg Val Pro						
				55		
					65	
acc gaa agg ggt tac cgc ctt ttt gtt gat tcc atc cat gac atc aaa						355
Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser Ile His Asp Ile Lys						
				70		
					85	
ccg ctg tgc ctg gcg gaa cgg cgc gct att ttg ggc ttc ctt gaa ggg						403
Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu Gly Phe Leu Glu Gly						
				90		
					100	
gga gtg gac tta gag gac gtg ctg cgc aga tct gtg cag ctg ttg tct						451
Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser Val Gln Leu Leu Ser						
				105		
					115	
cag ctc acc cat cag gct gcc gtg gtg cag ctg ccc acc ctg aaa aca						499
Gln Leu Thr His Gln Ala Ala Val Val Gln Leu Pro Thr Leu Lys Thr						
				120		
					130	
gcg cgc gtg aag cac tgc gag gtg gtg ccg ctg tgc ccg atg cgc ttg						547
Ala Arg Val Lys His Cys Glu Val Val Pro Leu Ser Pro Met Arg Leu						
				135		
					145	
ctg ctg gtg ctc att acc gat act ggc cgt gta gat cag cgc aac gtg						595
Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val Asp Gln Arg Asn Val						
				150		
					160	
gaa ctt gag gaa ccg ctg gcg gcg gaa gaa gtt aat gtg ctg cgc gat						643
Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val Asn Val Leu Arg Asp						
				170		
					180	
ctg ctc aac ggc gcg cta ggg gag aaa acg ctg acg gct gca tca gat						691
Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu Thr Ala Ala Ser Asp						
				185		
					195	
gcg ctg gaa gag ttg gct cag caa gcc cca acc gat att cgt gat gcc						739
Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr Asp Ile Arg Asp Ala						
				200		
					210	
atg cgc cgc tgc tgc gat gtg ctg gtg aac acg ctt gtc gat caa ccc						787
Met Arg Arg Cys Cys Asp Val Leu Val Asn Thr Leu Val Asp Gln Pro						
				215		
					225	
tct gac cgc ctg atc ctc gcc ggc acc tca aac ctc acc cgc tta agc						835
Ser Asp Arg Leu Ile Leu Ala Gly Thr Ser Asn Leu Thr Arg Leu Ser						

230	235	240	245	
cgg gaa acc tcc gcg agc ctg ccc atg gtt tta gaa gcc ttg gaa gag				883
Arg Glu Thr Ser	Ala Ser Leu Pro Met	Val Leu Glu Ala Leu	Glu Glu	
	250	255	260	
cag gtg gtc atg ttg aaa ctg ctg tcc aat gtc act gat ctt gac caa				931
Gln Val Val Met Leu Lys Leu Leu Ser Asn Val Thr Asp Leu Asp Gln				
	265	270	275	
gtg cgc gtg cat att ggc ggc gaa aat gaa gac att gag ctg cgc agc				979
Val Arg Val His Ile Gly Gly Glu Asn Glu Asp Ile Glu Leu Arg Ser				
	280	285	290	
gca acg gtg att acc acc ggt tac ggc tcc cag ggc agc gca ctg ggc				1027
Ala Thr Val Ile Thr Thr Gly Tyr Gly Ser Gln Gly Ser Ala Leu Gly				
	295	300	305	
gga ttg ggg gtg gtt ggc ccc acc tat atg gac tac tcg gga aca att				1075
Gly Leu Gly Val Val Gly Pro Thr Tyr Met Asp Tyr Ser Gly Thr Ile				
310	315	320	325	
tct aag gtg tcc gcc gtt gct aag tat gtt ggt cgt gtg ctc gct ggc				1123
Ser Lys Val Ser Ala Val Ala Lys Tyr Val Gly Arg Val Leu Ala Gly				
	330	335	340	
gaa tagctgcggg tatagttggc cat				1149
Glu				

<210> 122

<211> 342

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Met Val Ser Ala Thr Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile				
1	5	10	15	
Val Ala Asp Tyr Ile Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu				
	20	25	30	
Leu Glu Arg His Lys Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp				
	35	40	45	
Met Ser Val Leu Glu Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser				
	50	55	60	
Ser Gly Arg Val Pro Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser				
	65	70	75	80
Ile His Asp Ile Lys Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu				
	85	90	95	
Gly Phe Leu Glu Gly Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser				
	100	105	110	
Val Gln Leu Leu Ser Gln Leu Thr His Gln Ala Ala Val Val Gln Leu				
	115	120	125	

Pro Thr Leu Lys Thr Ala Arg Val Lys His Cys Glu Val Val Pro Leu
 130 135 140
 Ser Pro Met Arg Leu Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val
 145 150 155 160
 Asp Gln Arg Asn Val Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val
 165 170 175
 Asn Val Leu Arg Asp Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu
 180 185 190
 Thr Ala Ala Ser Asp Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr
 195 200 205
 Asp Ile Arg Asp Ala Met Arg Arg Cys Cys Asp Val Leu Val Asn Thr
 210 215 220
 Leu Val Asp Gln Pro Ser Asp Arg Leu Ile Leu Ala Gly Thr Ser Asn
 225 230 235 240
 Leu Thr Arg Leu Ser Arg Glu Thr Ser Ala Ser Leu Pro Met Val Leu
 245 250 255
 Glu Ala Leu Glu Glu Gln Val Val Met Leu Lys Leu Leu Ser Asn Val
 260 265 270
 Thr Asp Leu Asp Gln Val Arg Val His Ile Gly Gly Glu Asn Glu Asp
 275 280 285
 Ile Glu Leu Arg Ser Ala Thr Val Ile Thr Thr Gly Tyr Gly Ser Gln
 290 295 300
 Gly Ser Ala Leu Gly Gly Leu Gly Val Val Gly Pro Thr Tyr Met Asp
 305 310 315 320
 Tyr Ser Gly Thr Ile Ser Lys Val Ser Ala Val Ala Lys Tyr Val Gly
 325 330 335
 Arg Val Leu Ala Gly Glu
 340

<210> 123
 <211> 369
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(346)
 <223> RXA01418

<400> 123
 aacactcaaa tgatcatttg actattagcg aaagaaatta tcaatggagc atcaacctca 60

tctcctgaag ctcgccgatg agtgggcgcc aacattcaaa atg ctc ggc gat cgc 115
 Met Leu Gly Asp Arg
 1 5

acg cgc ctc cgc ctc ctc atc gcg ctg cat tat cac ggc ccc ggt gaa 163

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Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr His Gly Pro Gly Glu
      10                      15                      20

gcc acc gtc tca gaa ctc gcg gac atc gtc ggc gtc acc ctg ccc acg 211
Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly Val Thr Leu Pro Thr
      25                      30                      35

gcc tcc gca gcg ctc caa ctg ctc gca gat aac gga gtg gtc gag tcc 259
Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn Gly Val Val Glu Ser
      40                      45                      50

ttc aag gag ggg cgg gtg aca aga tat aag ctt gtc gac gcc acg acc 307
Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu Val Asp Ala Thr Thr
      55                      60                      65

cac acc ttg ctt cac cac ctc ggg ggc acc cac cga cat taaaggggaac 356
His Thr Leu Leu His His Leu Gly Gly Thr His Arg His
      70                      75                      80

caaatagcgt tcg 369

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<210> 124
 <211> 82
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 124
Met Leu Gly Asp Arg Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr
  1                      5                      10                      15

His Gly Pro Gly Glu Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly
      20                      25                      30

Val Thr Leu Pro Thr Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn
      35                      40                      45

Gly Val Val Glu Ser Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu
      50                      55                      60

Val Asp Ala Thr Thr His Thr Leu Leu His His Leu Gly Gly Thr His
      65                      70                      75                      80

Arg His

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<210> 125
 <211> 885
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(862)
 <223> RXA01759

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<400> 125
cactaaagaa cttctgagcg cgctatcggt ggtcgatgct attggtctgg gtacttctcc 60
ggtagaccat cactctgaat aaggggggata acatatagtt atg acc aaa cgg ctc 115

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											Met 1	Thr	Lys	Arg	Leu 5	
agc Ser	ctt Leu	gaa Glu	ggg Gly	ctc Leu 10	cgc Arg	tat Tyr	gcg Ala	cag Gln	gcc Ala 15	gtc Val	gca Ala	gaa Glu	act Thr	cac His 20	tca Ser	163
ttc Phe	agc Ser	gca Ala 25	gca Ala	gcc Ala	cgc Arg	gaa Glu	tac Tyr	gga Gly 30	gtc Val	acc Thr	caa Gln	cct Pro	gcg Ala 35	cta Leu	tcc Ser	211
aac Asn	ggc Gly 40	atc Ile	gcc Ala	aaa Lys	ctg Leu	gaa Glu	gat Asp 45	cgg Arg	ctc Leu	ggg Gly	gaa Glu	caa Gln 50	ctc Leu	ttc Phe	gat Asp	259
cga Arg	tct Ser 55	act Thr	caa Gln	ggc Gly	gtc Val	acc Thr 60	ccg Pro	acg Thr	tcc Ser	ttt Phe	ggc Gly 65	ctc Leu	cac His	atc Ile	ctc Leu	307
ccc Pro 70	ctg Leu	atc Ile	caa Gln	cgc Arg	gcg Ala 75	ctg Leu	act Thr	gaa Glu	atc Ile	gac Asp 80	gca Ala	atc Ile	acc Thr	gcg Ala	gaa Glu 85	355
gcg Ala	cac His	cgt Arg	ttg Leu	att Ile 90	aac Asn	tca Ser	gaa Glu	gca Ala	cgc Arg 95	agc Ser	att Ile	cga Arg	gtt Val	gga Gly 100	atc Ile	403
tcc Ser	cca Pro	ctt Leu	atc Ile 105	aac Asn	cct Pro	caa Gln	ctg Leu	gtt Val 110	gca Ala	cga Arg	aca Thr	tat Tyr	acc Thr 115	gcg Ala	gtt Val	451
cgt Arg	gag Glu	ctt Leu 120	ccc Pro	aca Thr	gca Ala	cac His	gac Asp 125	cta Leu	gta Val	ctc Leu	cgc Arg	gaa Glu 130	gca Ala	aac Asn	atg Met	499
aaa Lys	gaa Glu 135	cta Leu	cat His	gaa Glu	gga Gly	ctt Leu 140	ctt Leu	gca Ala	ggg Gly	gaa Glu	ctt Leu 145	aat Asn	gta Val	att Ile	ctc Leu	547
att Ile 150	ccc Pro	gca Ala	gtg Val	aaa Lys	cca Pro 155	cta Leu	ccc Pro	cat His	ttt Phe	gaa Glu 160	cac His	cgc Arg	atc Ile	att Ile	gac Asp 165	595
tcc Ser	gaa Glu	cca Pro	gtc Val	gtt Val 170	atc Ile	gtc Val	gaa Glu	tcc Ser	acc Thr 175	cag Gln	gac Asp	agc Ser	acc Thr	gac Asp 180	ccc Pro	643
ata Ile	gaa Glu	ctt Leu	cgc Arg 185	gag Glu	act Thr	cag Gln	cac His	gaa Glu 190	ccg Pro	ttc Phe	att Ile	ctg Leu	gta Val 195	ccc Pro	gac Asp	691
aca Thr	tgc Cys	ggg Gly 200	tta Leu	acc Thr	act Thr	ttc Phe	acc Thr 205	aat Asn	caa Gln	ctg Leu	ttt Phe	gaa Glu 210	aca Thr	aat Asn	gac Asp	739
ctg Leu	gca Ala 215	tta Leu	aac Asn	gcc Ala	tat Tyr	tcc Ser 220	ggc Gly	gaa Glu	gca Ala	gcc Ala	agc Ser 225	tac Tyr	caa Gln	gta Val	ctc Leu	787
gaa Glu	cag Gln	tgg Trp	gcc Ala	aca Thr	ctt Leu	gga Gly	ctc Leu	gga Gly	tct Ser	gca Ala	atg Met	ctt Leu	cca Pro	ctt Leu	tct Ser	835

230 235 240 245 885

aaa ctc agc tcc cct aca gca ccc cat tgaccactcc gcgaacaagg cct
Lys Leu Ser Ser Pro Thr Ala Pro His
250

<210> 126
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 126
Met Thr Lys Arg Leu Ser Leu Glu Gly Leu Arg Tyr Ala Gln Ala Val
1 5 10 15
Ala Glu Thr His Ser Phe Ser Ala Ala Ala Arg Glu Tyr Gly Val Thr
20 25 30
Gln Pro Ala Leu Ser Asn Gly Ile Ala Lys Leu Glu Asp Arg Leu Gly
35 40 45
Glu Gln Leu Phe Asp Arg Ser Thr Gln Gly Val Thr Pro Thr Ser Phe
50 55 60
Gly Leu His Ile Leu Pro Leu Ile Gln Arg Ala Leu Thr Glu Ile Asp
65 70 75 80
Ala Ile Thr Ala Glu Ala His Arg Leu Ile Asn Ser Glu Ala Arg Ser
85 90 95
Ile Arg Val Gly Ile Ser Pro Leu Ile Asn Pro Gln Leu Val Ala Arg
100 105 110
Thr Tyr Thr Ala Val Arg Glu Leu Pro Thr Ala His Asp Leu Val Leu
115 120 125
Arg Glu Ala Asn Met Lys Glu Leu His Glu Gly Leu Leu Ala Gly Glu
130 135 140
Leu Asn Val Ile Leu Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu
145 150 155 160
His Arg Ile Ile Asp Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln
165 170 175
Asp Ser Thr Asp Pro Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe
180 185 190
Ile Leu Val Pro Asp Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu
195 200 205
Phe Glu Thr Asn Asp Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala
210 215 220
Ser Tyr Gln Val Leu Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala
225 230 235 240
Met Leu Pro Leu Ser Lys Leu Ser Ser Pro Thr Ala Pro His
245 250

<400> 127																
tgaatttgat ggtgtgagtc atggtgggtc cttttgtgaa attcgatcca agcgggcttt																60
gagtaacatg ttaccgggta ctgtggtgaa ttgtgcgata											atg Met 1	tca Ser	gac Asp	atg Met	cca Pro 5	115
aca Thr	aaa Lys	agg Arg	gtt Val	gcc Ala 10	ccc Pro	gca Ala	cgc Arg	tca Ser	ctc Leu 15	acc Thr	gac Asp	caa Gln	gtc Val	atg Met 20	gat Asp	163
ttc gtc cgc gaa tcc acc ctt gat aaa				aca atg gtc acc gga gag tgg								211				
Phe Val Arg Glu Ser Thr Leu Asp Lys				Thr Met Val Thr Gly Glu Trp												
25				30				35								
tac agc gtt tac cag gtc agc gac caa tta ggc att tcc cgc tcc ccc																259
Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly Ile Ser Arg Ser Pro																
40				45				50								
gtc aga gac gcg ctg ctc cgc ctg gaa gaa gca ggg ctc atc cgc ttc																307
Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala Gly Leu Ile Arg Phe																
55				60				65								
acc agg aac cgc gga ttc caa att gtc gaa acc aaa ccc tct gat gtc																355
Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr Lys Pro Ser Asp Val																
70				75				80				85				
gcc gaa att ttt gcc ctt cgt cta ggc att gaa ccc gcc gca gca tac																403
Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu Pro Ala Ala Ala Tyr																
90				95				100								
cgg gca gca cag cta cgc acc gaa gaa cag ctc cac gaa gca gat gac																451
Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu His Glu Ala Asp Asp																
105				110				115								
atc att gca ctc atg gcg caa gcc gag gcc gac aat gac gaa gaa gca																499
Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp Asn Asp Glu Glu Ala																
120				125				130								
ttt ttc acc cat gac cgg cag ttt cac cga caa att atg acc atg gga																547
Phe Phe Thr His Asp Arg Gln Phe His Arg Gln Ile Met Thr Met Gly																
135				140				145								
cac tcc caa cgc ggg gct gac ctg gta gaa aaa cta cgc gca cac acc																595
His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys Leu Arg Ala His Thr																
150				155				160				165				
cgt atc ctc ggt gct tct act gcc ggg aac aaa cgc acc ctt ggc gat																643
Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys Arg Thr Leu Gly Asp																
170				175				180								

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att ttg gaa gaa cac gaa cca atc ttg gat gcc atc aaa cga caa tca 691
Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala Ile Lys Arg Gln Ser
      185                      190                      195

gca gaa atg gca cga gcc acc atg cgg gag cat atc caa gtc acc gga 739
Ala Glu Met Ala Arg Ala Thr Met Arg Glu His Ile Gln Val Thr Gly
      200                      205                      210

aag cta cta cta gaa caa gca gtg gaa aaa tcc ggc gaa gga gct gct 787
Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser Gly Glu Gly Ala Ala
      215                      220                      225

cag aag att tgg gat cag tac acg gcg gga gtt taggcatatt tacctaataca 840
Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
      230                      235                      240

att 843

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<210> 128
<211> 240
<212> PRT
<213> Corynebacterium glutamicum

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<400> 128
Met Ser Asp Met Pro Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr
  1          5          10          15

Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met
      20          25          30

Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly
      35          40          45

Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala
      50          55          60

Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr
      65          70          75          80

Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu
      85          90          95

Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu
      100         105         110

His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp
      115         120         125

Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln Phe His Arg Gln
      130         135         140

Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys
      145         150         155         160

Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys
      165         170         175

Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala
      180         185         190

```

Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr Met Arg Glu His
 195 200 205

Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser
 210 215 220

Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
 225 230 235 240

<210> 129

<211> 707

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(684)

<223> FRXA00363

<400> 129

cgc tca ctc acc gac caa gtc atg gat ttc gtc cgc gaa tcc acc ctt 48
 Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu
 1 5 10 15

gat aaa aca atg gtc acc gga gag tgg tac agc gtt tac cag gtc agc 96
 Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
 20 25 30

gac caa tta ggc att tcc cgc tcc ccc gtc aga gac gcg ctg ctc cgc 144
 Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
 35 40 45

ctg gaa gaa gca ggg ctc atc cgc ttc acc agg aac cgc gga ttc caa 192
 Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
 50 55 60

att gtc gaa acc aaa ccc tct gat gtc gcc gaa att ttt gcc ctt cgt 240
 Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
 65 70 75 80

cta ggc att gaa ccc gcc gca gca tac cgg gca gca cag cta cgc acc 288
 Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
 85 90 95

gaa gaa cag ctc cac gaa gca gat gac atc att gca ctc atg gcg caa 336
 Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
 100 105 110

gcc gag gcc gac aat gac gaa gaa gca ttt ttc acc cat gac cgg cag 384
 Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln
 115 120 125

ttt cac cga caa att atg acc atg gga cac tcc caa cgc ggg gct gac 432
 Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp
 130 135 140

ctg gta gaa aaa cta cgc gca cac acc cgt atc ctc ggt gct tct act 480
 Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr
 145 150 155 160

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gcc ggg aac aaa cgc acc ctt ggc gat att ttg gaa gaa cac gaa cca 528
Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro
      165                      170                      175

atc ttg gat gcc atc aaa cga caa tca gca gaa atg gca cga gcc acc 576
Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr
      180                      185                      190

atg cgg gag cat atc caa gtc acc gga aag cta cta cta gaa caa gca 624
Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala
      195                      200                      205

gtg gaa aaa tcc ggc gaa gga gct gct cag aag att tgg gat cag tac 672
Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr
      210                      215                      220

acg gcg gga gtt taggcatatt tacctaataca att 707
Thr Ala Gly Val
225

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<210> 130
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

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<400> 130
Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu
 1              5              10              15

Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
      20              25              30

Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg
      35              40              45

Leu Glu Glu Ala Gly Leu Ile Arg Phe Thr Arg Asn Arg Gly Phe Gln
      50              55              60

Ile Val Glu Thr Lys Pro Ser Asp Val Ala Glu Ile Phe Ala Leu Arg
      65              70              75              80

Leu Gly Ile Glu Pro Ala Ala Ala Tyr Arg Ala Ala Gln Leu Arg Thr
      85              90              95

Glu Glu Gln Leu His Glu Ala Asp Asp Ile Ile Ala Leu Met Ala Gln
      100             105             110

Ala Glu Ala Asp Asn Asp Glu Glu Ala Phe Phe Thr His Asp Arg Gln
      115             120             125

Phe His Arg Gln Ile Met Thr Met Gly His Ser Gln Arg Gly Ala Asp
      130             135             140

Leu Val Glu Lys Leu Arg Ala His Thr Arg Ile Leu Gly Ala Ser Thr
      145             150             155             160

Ala Gly Asn Lys Arg Thr Leu Gly Asp Ile Leu Glu Glu His Glu Pro
      165             170             175

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Ile Leu Asp Ala Ile Lys Arg Gln Ser Ala Glu Met Ala Arg Ala Thr
 180 185 190

Met Arg Glu His Ile Gln Val Thr Gly Lys Leu Leu Leu Glu Gln Ala
 195 200 205

Val Glu Lys Ser Gly Glu Gly Ala Ala Gln Lys Ile Trp Asp Gln Tyr
 210 215 220

Thr Ala Gly Val
 225

<210> 131
 <211> 843
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(820)
 <223> RXA00516

<400> 131
 aagcaaaaaa ttgcttgctg acgtctcccc caacctagca tccactttct gcaaccaggt 60

gtcacaaata gtctaaattt cgggtgtacta aggtgttgct atg gtc caa aaa gat 115
 Met Val Gln Lys Asp
 1 5

gcc cag gcc tcc cct gct acg aga aaa gca gat cag gta tac aca cag 163
 Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp Gln Val Tyr Thr Gln
 10 15 20

att cgt cgt gaa atc gaa gat gga acc tta aat cct ggg caa cga atg 211
 Ile Arg Arg Glu Ile Glu Asp Gly Thr Leu Asn Pro Gly Gln Arg Met
 25 30 35

tcg gaa gtg tgg ctg gtt gaa cac acc ggc gct tcg aga acc cca gtc 259
 Ser Glu Val Trp Leu Val Glu His Thr Gly Ala Ser Arg Thr Pro Val
 40 45 50

cgg gat gct ctg cgc cgg tta gcc gca gac gag ttg atc att ttg gag 307
 Arg Asp Ala Leu Arg Arg Leu Ala Ala Asp Glu Leu Ile Ile Leu Glu
 55 60 65

cca cgt cag gcg cct atg gtg tcg cca ctt tcg ctt cgc cac att aag 355
 Pro Arg Gln Ala Pro Met Val Ser Pro Leu Ser Leu Arg His Ile Lys
 70 75 80 85

gat ctg ttt gag ttc cgc agg atc gtc gag gtc gca gcg ctt gag gaa 403
 Asp Leu Phe Glu Phe Arg Arg Ile Val Glu Val Ala Ala Leu Glu Glu
 90 95 100

atc tct gtt gga gcg agt aaa tca ccg cgt atc ttt ggt gag ttt tct 451
 Ile Ser Val Gly Ala Ser Lys Ser Pro Arg Ile Phe Gly Glu Phe Ser
 105 110 115

acg ttg gcg gca gat ttt cga gag ctg gaa aac tct gca gac gat gca 499
 Thr Leu Ala Ala Asp Phe Arg Glu Leu Glu Asn Ser Ala Asp Asp Ala
 120 125 130

gat ttc acc gcc gat ttt agg cga ttg acc agt aag ttt gat gat ctt 547
Asp Phe Thr Ala Asp Phe Arg Arg Leu Thr Ser Lys Phe Asp Asp Leu
135 140 145

gtt gca gca aat act cac aac caa ttc ctt gga cgc agc atc tta agt 595
Val Ala Ala Asn Thr His Asn Gln Phe Leu Gly Arg Ser Ile Leu Ser
150 155 160 165

tta aaa ccg cac acc acg agg ctg cgg atc att gcg cat tcc gat cat 643
Leu Lys Pro His Thr Thr Arg Leu Arg Ile Ile Ala His Ser Asp His
170 175 180

gcg cgt ctg cgc caa tcg gtt cag gaa cat att gaa atg tgt gaa gct 691
Ala Arg Leu Arg Gln Ser Val Gln Glu His Ile Glu Met Cys Glu Ala
185 190 195

gtg gcc tca gga gat tta agg tcg gca ggc gct gcg tgt aga cag cac 739
Val Ala Ser Gly Asp Leu Arg Ser Ala Gly Ala Ala Cys Arg Gln His
200 205 210

ctg atc cat gta gaa aag agc att ttg acc gca ttg att aat gct gat 787
Leu Ile His Val Glu Lys Ser Ile Leu Thr Ala Leu Ile Asn Ala Asp
215 220 225

tct acg ggc tcg cag ggc att gat att agg tct tagaaccagc gtgcactgat 840
Ser Thr Gly Ser Gln Gly Ile Asp Ile Arg Ser
230 235 240

ggc 843

<210> 132

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Val Gln Lys Asp Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp
1 5 10 15

Gln Val Tyr Thr Gln Ile Arg Arg Glu Ile Glu Asp Gly Thr Leu Asn
20 25 30

Pro Gly Gln Arg Met Ser Glu Val Trp Leu Val Glu His Thr Gly Ala
35 40 45

Ser Arg Thr Pro Val Arg Asp Ala Leu Arg Arg Leu Ala Ala Asp Glu
50 55 60

Leu Ile Ile Leu Glu Pro Arg Gln Ala Pro Met Val Ser Pro Leu Ser
65 70 75 80

Leu Arg His Ile Lys Asp Leu Phe Glu Phe Arg Arg Ile Val Glu Val
85 90 95

Ala Ala Leu Glu Glu Ile Ser Val Gly Ala Ser Lys Ser Pro Arg Ile
100 105 110

Phe Gly Glu Phe Ser Thr Leu Ala Ala Asp Phe Arg Glu Leu Glu Asn
115 120 125

Ser Ala Asp Asp Ala Asp Phe Thr Ala Asp Phe Arg Arg Leu Thr Ser
 130 135 140

Lys Phe Asp Asp Leu Val Ala Ala Asn Thr His Asn Gln Phe Leu Gly
 145 150 155 160

Arg Ser Ile Leu Ser Leu Lys Pro His Thr Thr Arg Leu Arg Ile Ile
 165 170 175

Ala His Ser Asp His Ala Arg Leu Arg Gln Ser Val Gln Glu His Ile
 180 185 190

Glu Met Cys Glu Ala Val Ala Ser Gly Asp Leu Arg Ser Ala Gly Ala
 195 200 205

Ala Cys Arg Gln His Leu Ile His Val Glu Lys Ser Ile Leu Thr Ala
 210 215 220

Leu Ile Asn Ala Asp Ser Thr Gly Ser Gln Gly Ile Asp Ile Arg Ser
 225 230 235 240

<210> 133
 <211> 774
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(751)
 <223> RXA01537

<400> 133
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aagtgcctag gtgtgtcccc agtcctttaa gatcagtcac atg acg cag gca ata 115
 Met Thr Gln Ala Ile
 1 5

gca gca tcc ctt gat tta gcg gct cga atc acc gcc aaa att gat caa 163
 Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr Ala Lys Ile Asp Gln
 10 15 20

gga gtg ctc act cca ggt act cga cta ccc gag gtt gct ttg gca gaa 211
 Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu Val Ala Leu Ala Glu
 25 30 35

gaa ctt ggc gtt tca cgg aac acg ctg cgt gaa gct ttt cgg gta ctc 259
 Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu Ala Phe Arg Val Leu
 40 45 50

atg caa gac gga ctg gtg gat cat att ccc aac cgt ggg gtt ttc gtg 307
 Met Gln Asp Gly Leu Val Asp His Ile Pro Asn Arg Gly Val Phe Val
 55 60 65

cac acg ttc acc aag tcg gat gtg gaa gat atc tat gct tac cgc aca 355
 His Thr Phe Thr Lys Ser Asp Val Glu Asp Ile Tyr Ala Tyr Arg Thr
 70 75 80 85

ttt atc gag gtt gct gcg att agg tcg gcg cgg aaa aat cct cag ttg 403

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<400> 134
Met Thr Gln Ala Ile Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr
  1          5          10          15

Ala Lys Ile Asp Gln Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu
          20          25          30

Val Ala Leu Ala Glu Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu
      35          40          45

Ala Phe Arg Val Leu Met Gln Asp Gly Leu Val Asp His Ile Pro Asn
      50          55          60

Arg Gly Val Phe Val His Thr Phe Thr Lys Ser Asp Val Glu Asp Ile
  65          70          75          80

Tyr Ala Tyr Arg Thr Phe Ile Glu Val Ala Ala Ile Arg Ser Ala Arg
          85          90          95

Lys Asn Pro Gln Leu Leu Glu Gln Ser Leu Gly Val Met Arg Glu Ala

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<210> 135
<211> 819
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(796)
<223> RXA02494
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 Asp Lys Val Val Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys
 90 95 100

cca tat tct tcc cgc gaa ctc atc gcc cgc atc cgc gct gtc ctg cgc 451
 Pro Tyr Ser Ser Arg Glu Leu Ile Ala Arg Ile Arg Ala Val Leu Arg
 105 110 115

cga cgc gga gtt act gaa acc gaa gcc gaa gaa tta cca ctt gac gat 499
 Arg Arg Gly Val Thr Glu Thr Glu Ala Glu Glu Leu Pro Leu Asp Asp
 120 125 130

caa atc ctc gaa ggc ggc cgc gtc cgc atg gac gtc gat tcc cac acc 547
 Gln Ile Leu Glu Gly Gly Arg Val Arg Met Asp Val Asp Ser His Thr
 135 140 145

gtc acc gtc ggt ggc gaa cca gtg agc atg cca ctg aag gaa ttc gac 595
 Val Thr Val Gly Gly Glu Pro Val Ser Met Pro Leu Lys Glu Phe Asp
 150 155 160 165

ctt ctg gag tac ctc ctc cga aac gcc ggc cga gtc ctc acc cgc gga 643
 Leu Leu Glu Tyr Leu Leu Arg Asn Ala Gly Arg Val Leu Thr Arg Gly
 170 175 180

cag ctc atc gac cga att tgg ggc gca gat tac gtc ggc gac acc aaa 691
 Gln Leu Ile Asp Arg Ile Trp Gly Ala Asp Tyr Val Gly Asp Thr Lys
 185 190 195

acc ctc gac gtt cat gtc aaa agg ttg cgt tcc aag atc gaa gaa gag 739
 Thr Leu Asp Val His Val Lys Arg Leu Arg Ser Lys Ile Glu Glu Glu
 200 205 210

cca tct cgc cct cgt tac ctc gtg acc gtg cgt gga ttg ggc tac aaa 787
 Pro Ser Arg Pro Arg Tyr Leu Val Thr Val Arg Gly Leu Gly Tyr Lys
 215 220 225

ttc gag ctg tagggctctg ttagggccctg ttg 819
 Phe Glu Leu
 230

<210> 136

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Thr Arg Ile Leu Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro
 1 5 10 15

Leu Ala Phe Leu Leu Arg Lys Glu Gly Phe Asp Thr Ile Ile Ala Gly
 20 25 30

Asp Gly Pro Thr Ala Leu Val Glu Phe Ser Arg Asn Glu Ile Asp Ile
 35 40 45

Val Leu Leu Asp Leu Met Leu Pro Gly Met Ser Gly Thr Asp Val Cys
 50 55 60

Lys Glu Leu Arg Ser Val Ser Thr Val Pro Val Ile Met Val Thr Ala
 65 70 75 80

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<210> 137
<211> 660
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(637)  
<223> RXA00029
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<400> 137																	
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ttgccgt	gcg	ccaggt	gagg	accgag	aggc	caaac	gcatt	ttg	gcc	cag	gcc	acc	115				
								Leu	Ala	Gln	Ala	Thr					
								1				5					
gcc	caa	cta	atc	gct	gat	gat	gaa	gca	gta	att	ttc	gac	aac	ggc	acc	163	
Ala	Gln	Leu	Ile	Ala	Asp	Asp	Glu	Ala	Val	Ile	Phe	Asp	Asn	Gly	Thr		
				10					15					20			
acc	tgc	cag	gca	gtg	gcc	caa	gag	ttg	gcg	ggg	cgt	ccc	atc	acg	gca	211	
Thr	Cys	Gln	Ala	Val	Ala	Gln	Glu	Leu	Ala	Gly	Arg	Pro	Ile	Thr	Ala		
			25					30					35				
ttg	tgt	ctg	tct	cta	cat	tcg	gcg	gtc	gcc	ctg	gga	agc	cga	gct	ggc	259	
Leu	Cys	Leu	Ser	Leu	His	Ser	Ala	Val	Ala	Leu	Gly	Ser	Arg	Ala	Gly		
		40					45					50					

acc aac gtt ttc atc ccc ggc ggc ccc gtg gaa aac gac tca ctc gcc 307
 Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu Asn Asp Ser Leu Ala
 55 60 65

tta tct ggc ccg gct gtg atc acc gcg tta cga gat ttc tcc gcc gat 355
 Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg Asp Phe Ser Ala Asp
 70 75 80 85

gtc gtg atc ctc ggt tcc tgc tct aca tca ctg gag cac ggg ttg gcc 403
 Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu Glu His Gly Leu Ala
 90 95 100

acc act acc tac gac gat gcg gaa aac aag cgc gca gcc atc cat gct 451
 Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg Ala Ala Ile His Ala
 105 110 115

gcc acc cga cga atc ctt gtg gtg tcc gcc cgt aaa ctc aac cac gtt 499
 Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg Lys Leu Asn His Val
 120 125 130

tcc act ttc cgt ttc gca gac gtc gcg gac tta cac cag ctg gtc aca 547
 Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu His Gln Leu Val Thr
 135 140 145

acc tcc gat gcg cca cgg gag att ctc gcc gag atc cgg gat ctc ggc 595
 Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu Ile Arg Asp Leu Gly
 150 155 160 165

gtg cag gtt att act gtt ccc gcc cct gac gag caa cga agt 637
 Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu Gln Arg Ser
 170 175

taactcttca tgggtgctga gca 660

<210> 138
 <211> 179
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 138
 Leu Ala Gln Ala Thr Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile
 1 5 10 15

Phe Asp Asn Gly Thr Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly
 20 25 30

Arg Pro Ile Thr Ala Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu
 35 40 45

Gly Ser Arg Ala Gly Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu
 50 55 60

Asn Asp Ser Leu Ala Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg
 65 70 75 80

Asp Phe Ser Ala Asp Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu
 85 90 95

Glu His Gly Leu Ala Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg
 100 105 110

Ala Ala Ile His Ala Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg
 115 120 125

Lys Leu Asn His Val Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu
 130~ 135 140

His Gln Leu Val Thr Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu
 145 150 155 160

Ile Arg Asp Leu Gly Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu
 165 170 175

Gln Arg Ser

<210> 139
 <211> 762
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(739)
 <223> RXA00655

<400> 139
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gtatcttgaa acagaccaac ccgaaaggac gtggccgaac gtg gct gct agc gct 115
 Val Ala Ala Ser Ala
 1 5

tca ggc aag agt aaa aca agt gcc ggg gca aac cgt cgt cgc aat cga 163
 Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn Arg Arg Arg Asn Arg
 10 15 20

cca agc ccc cga cag cgt ctc ctc gat agc gca acc aac ctt ttc acc 211
 Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala Thr Asn Leu Phe Thr
 25 30 35

aca gaa ggt att cgc gtc atc ggt att gat cgt atc ctc cgt gaa gct 259
 Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg Ile Leu Arg Glu Ala
 40 45 50

gac gtg gcg aag gcg agc ctc tat tcc ctt ttc gga tcg aag gac gcc 307
 Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe Gly Ser Lys Asp Ala
 55 60 65

ttg gtt att gca tac ctg gag aac ctc gat cag ctg tgg cgt gaa gcg 355
 Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln Leu Trp Arg Glu Ala
 70 75 80 85

tgg cgt gag cgc acc gtc ggt atg aag gat ccg gaa gat aaa atc atc 403
 Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro Glu Asp Lys Ile Ile
 90 95 100

gcg ttc ttt gat cag tgc att gag gaa gaa cca gaa aaa gat ttc cgc 451
 Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro Glu Lys Asp Phe Arg
 105 110 115

ggc tcg cac ttt cag aat gcg gct agt gag tac cct cgc ccc gaa act 499
 Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr Pro Arg Pro Glu Thr
 120 125 130

gat agc gaa aag ggc att gtt gca gca gtg tta gag cac cgc gag tgg 547
 Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu Glu His Arg Glu Trp
 135 140 145

tgt cat aag act ctg act gat ttg ctc act gag aag aac ggc tac cca 595
 Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu Lys Asn Gly Tyr Pro
 150 155 160 165

ggc acc acc cag gcg aat cag ctg ttg gtg ttc ctt gat ggt gga ctt 643
 Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe Leu Asp Gly Gly Leu
 170 175 180

gct gga tct cga ttg gtc cac aac atc agt cct ctt gag acg gct cgc 691
 Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro Leu Glu Thr Ala Arg
 185 190 195

gat ttg gct cgg cag ttg ttg tcg gct cca cct gcg gac tac tca att 739
 Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro Ala Asp Tyr Ser Ile
 200 205 210

tagttttcttc attttccgaa ggg 762

<210> 140

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Val Ala Ala Ser Ala Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn
 1 5 10 15

Arg Arg Arg Asn Arg Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala
 20 25 30

Thr Asn Leu Phe Thr Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg
 35 40 45

Ile Leu Arg Glu Ala Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe
 50 55 60

Gly Ser Lys Asp Ala Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln
 65 70 75 80

Leu Trp Arg Glu Ala Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro
 85 90 95

Glu Asp Lys Ile Ile Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro
 100 105 110

Glu Lys Asp Phe Arg Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr
 115 120 125

Pro Arg Pro Glu Thr Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu
 130 135 140

Glu His Arg Glu Trp Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu
 145 150 155 160
 Lys Asn Gly Tyr Pro Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe
 165 170 175
 Leu Asp Gly Gly Leu Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro
 180 185 190
 Leu Glu Thr Ala Arg Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro
 195 200 205
 Ala Asp Tyr Ser Ile
 210

<210> 141
 <211> 2538
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2515)
 <223> RXN03136

<400> 141
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 Leu Gly Ala His Ser
 1 5
 gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg 163
 Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val
 10 15 20
 gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa 211
 Val Ile Val Ala Asp Val His Trp Ala Asp Val Glu Ser Met Gln Lys
 25 30 35
 ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc 259
 Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly Arg Phe Ala Leu Ile
 40 45 50
 atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc 307
 Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe His Asp Glu Val Val
 55 60 65
 tcg ctc ccc tcc atc gca gac tcc acc tac gta ttg ccg ccg atg agt 355
 Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val Leu Pro Pro Met Ser
 70 75 80 85
 att gaa gaa atc cgc cag ctt gcg ctt acc gat gtc cgc ggc cgc atc 403
 Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp Val Arg Gly Arg Ile
 90 95 100
 agc acc acc acc gcc aca gac atc cag cgc atc acc ggc ggc atc tac 451
 Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile Thr Gly Gly Ile Tyr
 105 110 115

ggg cga gtc aaa gaa gtc ctc cac tcg gaa tcc ccc gat cac tgg cga	499
Gly Arg Val Lys Glu Val Leu His Ser Glu Ser Pro Asp His Trp Arg	
120 125 130	
atg ccc aac cca aat att ccc atc cca caa agc tgg cat gcc aac ctg	547
Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser Trp His Ala Asn Leu	
135 140 145	
ttg aga cgc atc acc aac gaa gaa gtc tgg cat gta cta ctc gcc gtc	595
Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His Val Leu Leu Ala Val	
150 155 160 165	
gct gtc ctt ccc tcc gga ggc ccc att gac ctg gta aaa ctc ata ggc	643
Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu Val Lys Leu Ile Gly	
170 175 180	
aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg	691
Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala Val Arg Ser Gly Leu	
185 190 195	
ctc cgc gtg ctg ccg tct gac ggc caa cca caa gtg gat ttg gtc ctg	739
Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln Val Asp Leu Val Leu	
200 205 210	
ccg atc gac cgc gcc gta ctg caa tca cgc act ccg ctc aac att ctg	787
Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr Pro Leu Asn Ile Leu	
215 220 225	
gcg cag ttg cac cac aag gca gcc gaa tat tac ggc aag tgg aat caa	835
Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr Gly Lys Trp Asn Gln	
230 235 240 245	
aaa gat gcc caa ctg gag cac gaa gca ttt gct gca att gat cca aat	883
Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala Ala Ile Asp Pro Asn	
250 255 260	
gat cca gca gtg cga gcc cta gcg cag cgc gga tat gcg ttg ggt agg	931
Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly Tyr Ala Leu Gly Arg	
265 270 275	
act ggc cac tgg atg gaa tcg gca cac gcc cta tct ctt gcc gcg aac	979
Thr Gly His Trp Met Glu Ser Ala His Ala Leu Ser Leu Ala Ala Asn	
280 285 290	
cgc act gca cac caa gaa gaa tca aat aag tac ttg ctg gag tcc atc	1027
Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr Leu Leu Glu Ser Ile	
295 300 305	
gat tca ctg atc gcc gcc gcc gat ctc ccc caa gct cga tcc aga gca	1075
Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln Ala Arg Ser Arg Ala	
310 315 320 325	
tcc acc ctt gat ctt gga gaa acc ggc att caa caa gac tca atg ctg	1123
Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln Gln Asp Ser Met Leu	
330 335 340	
ggc tac ctg gca atc cac gaa ggc cgg cgc ctc gaa gca cgc aat ctc	1171
Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu Glu Ala Arg Asn Leu	
345 350 355	
ctt cat cgt gct tct gaa gaa ttg ctg gcg cag cac ccg att gat ccg	1219

Leu	His	Arg	Ala	Ser	Glu	Glu	Leu	Leu	Ala	Gln	His	Pro	Ile	Asp	Pro		
		360					365					370					
atc	cac	ggc	ccc	cgc	atg	gct	cag	cgc	aaa	gta	ctg	tta	aac	tta	gtg		1267
Ile	His	Gly	Pro	Arg	Met	Ala	Gln	Arg	Lys	Val	Leu	Leu	Asn	Leu	Val		
		375				380					385						
gac	tgg	aat	cca	gaa	gaa	ctc	ctg	gtg	tgg	gct	gat	aga	gca	gtc	gca		1315
Asp	Trp	Asn	Pro	Glu	Glu	Leu	Leu	Val	Trp	Ala	Asp	Arg	Ala	Val	Ala		
390					395					400					405		
tgg	act	gaa	gag	gat	gct	ggc	gaa	aag	gtt	gag	gcc	caa	gct	att	tcc		1363
Trp	Thr	Glu	Glu	Asp	Ala	Gly	Glu	Lys	Val	Glu	Ala	Gln	Ala	Ile	Ser		
				410					415					420			
ctc	att	gga	caa	tcc	atc	ctc	gat	ggc	tgc	ctc	ccc	gaa	gat	aaa	ccc		1411
Leu	Ile	Gly	Gln	Ser	Ile	Leu	Asp	Gly	Cys	Leu	Pro	Glu	Asp	Lys	Pro		
			425					430					435				
atc	ccc	ggt	gaa	acc	acc	ctt	cac	gca	caa	cgc	cgc	cac	atg	gca	atg		1459
Ile	Pro	Gly	Glu	Thr	Thr	Leu	His	Ala	Gln	Arg	Arg	His	Met	Ala	Met		
		440					445					450					
ggc	tgg	ctt	tcc	atg	gtt	cac	gat	gat	cca	gta	act	gca	cgt	caa	aag		1507
Gly	Trp	Leu	Ser	Met	Val	His	Asp	Asp	Pro	Val	Thr	Ala	Arg	Gln	Lys		
	455					460					465						
ctt	gaa	cgt	cgc	aca	tcc	atc	aat	ggt	tca	gaa	cgc	atc	agt	ttg	tgg		1555
Leu	Glu	Arg	Arg	Thr	Ser	Ile	Asn	Gly	Ser	Glu	Arg	Ile	Ser	Leu	Trp		
470					475					480					485		
caa	gac	gga	tgg	ctg	gct	cgg	tcc	cta	ctg	ctg	ctc	ggc	gaa	tgg	gag		1603
Gln	Asp	Gly	Trp	Leu	Ala	Arg	Ser	Leu	Leu	Leu	Leu	Gly	Glu	Trp	Glu		
				490					495					500			
tcc	gca	gca	cgc	acc	gta	gaa	atc	ggt	ctg	gcc	cgc	gcc	gaa	cag	ttt		1651
Ser	Ala	Ala	Arg	Thr	Val	Glu	Ile	Gly	Leu	Ala	Arg	Ala	Glu	Gln	Phe		
			505					510					515				
ggc	atc	cgc	ttc	ctc	gaa	cca	ctg	tta	ctg	tgg	tcg	ggc	gcc	aca	att		1699
Gly	Ile	Arg	Phe	Leu	Glu	Pro	Leu	Leu	Leu	Trp	Ser	Gly	Ala	Thr	Ile		
		520					525					530					
gca	aca	gcc	cgc	gga	aac	tct	gac	ttg	gca	cga	aat	tac	atg	agc	aga		1747
Ala	Thr	Ala	Arg	Gly	Asn	Ser	Asp	Leu	Ala	Arg	Asn	Tyr	Met	Ser	Arg		
		535				540					545						
ctg	tcc	acc	gat	caa	gac	tcc	ttc	atc	gtc	caa	tct	atg	cca	tct	gcg		1795
Leu	Ser	Thr	Asp	Gln	Asp	Ser	Phe	Ile	Val	Gln	Ser	Met	Pro	Ser	Ala		
550					555					560					565		
atg	tgt	cgc	atg	tgg	gtc	cac	cgc	cat	aga	aat	gaa	atc	ccc	ggt	gcg		1843
Met	Cys	Arg	Met	Trp	Val	His	Arg	His	Arg	Asn	Glu	Ile	Pro	Gly	Ala		
				570					575					580			
atc	gtg	gcc	gga	gaa	caa	ttg	gaa	aaa	atc	gcc	gca	cac	aaa	cac	gtc		1891
Ile	Val	Ala	Gly	Glu	Gln	Leu	Glu	Lys	Ile	Ala	Ala	His	Lys	His	Val		
			585					590					595				
aac	gca	cct	gga	ttc	tgg	cca	tgg	caa	gac	gtc	cac	gca	acg	cat	ctc		1939
Asn	Ala	Pro	Gly	Phe	Trp	Pro	Trp	Gln	Asp	Val	His	Ala	Thr	His	Leu		

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atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr 615 620 625			1987
ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile 630 635 640 645			2035
gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys 650 655 660			2083
gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr 665 670 675			2131
ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu 680 685 690			2179
aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala 695 700 705			2227
gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala 710 715 720 725			2275
aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala 730 735 740			2323
ggt ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser 745 750 755			2371
ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys 760 765 770			2419
acc gtg gaa tac cat ctc acc cgg gtg tac aaa aag ctc gga ata cgc Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Ile Arg 775 780 785			2467
aat cgg atg gaa ctt gcc gag gct ttg aag aag tac tca cac gac gcc Asn Arg Met Glu Leu Ala Glu Ala Leu Lys Lys Tyr Ser His Asp Ala 790 795 800 805			2515
tagcagcggga tatgtttgcg gac			2538

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<211> 805

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

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Asp Ala Ser Thr Val Val Ile Val Ala Asp Val His Trp Ala Asp Val
 20 25 30
 Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly
 35 40 45
 Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe
 50 55 60
 His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val
 65 70 75 80
 Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp
 85 90 95
 Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile
 100 105 110
 Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser
 115 120 125
 Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser
 130 135 140
 Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His
 145 150 155 160
 Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu
 165 170 175
 Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala
 180 185 190
 Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln
 195 200 205
 Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr
 210 215 220
 Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr
 225 230 235 240
 Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala
 245 250 255
 Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly
 260 265 270
 Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu
 275 280 285
 Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr
 290 295 300
 Leu Leu Glu Ser Ile Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln
 305 310 315 320
 Ala Arg Ser Arg Ala Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln
 325 330 335

Gln Asp Ser Met Leu Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu
 340 345 350
 Glu Ala Arg Asn Leu Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln
 355 360 365
 His Pro Ile Asp Pro Ile His Gly Pro Arg Met Ala Gln Arg Lys Val
 370 375 380
 Leu Leu Asn Leu Val Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala
 385 390 395 400
 Asp Arg Ala Val Ala Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu
 405 410 415
 Ala Gln Ala Ile Ser Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu
 420 425 430
 Pro Glu Asp Lys Pro Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg
 435 440 445
 Arg His Met Ala Met Gly Trp Leu Ser Met Val His Asp Asp Pro Val
 450 455 460
 Thr Ala Arg Gln Lys Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu
 465 470 475 480
 Arg Ile Ser Leu Trp Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu
 485 490 495
 Leu Gly Glu Trp Glu Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala
 500 505 510
 Arg Ala Glu Gln Phe Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp
 515 520 525
 Ser Gly Ala Thr Ile Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg
 530 535 540
 Asn Tyr Met Ser Arg Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln
 545 550 555 560
 Ser Met Pro Ser Ala Met Cys Arg Met Trp Val His Arg His Arg Asn
 565 570 575
 Glu Ile Pro Gly Ala Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala
 580 585 590
 Ala His Lys His Val Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val
 595 600 605
 His Ala Thr His Leu Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu
 610 615 620
 Leu Val Asn Ser Thr Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser
 625 630 635 640
 Ala His Ala Lys Ile Ala Val Pro Asp Ala Met Leu Met Ile His His
 645 650 655
 Gly Asp Val Lys Lys Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met

660							665					670				
Ile	Asp	Pro	Leu	Thr	Leu	Pro	Tyr	Tyr	Arg	Ala	Arg	Ile	Cys	Phe	Glu	
		675					680					685				
Tyr	Gly	Gln	Ala	Leu	Arg	Arg	Gln	Gly	Gln	Arg	Arg	Arg	Ala	Asp	Glu	
	690					695					700					
Gln	Phe	Ala	Arg	Ala	Ala	Ser	Leu	Phe	Gln	Asp	Met	Gly	Ala	Asp	Ala	
705					710					715					720	
Met	Val	Thr	Leu	Ala	Asn	Arg	Glu	Arg	Arg	Val	Gly	Gly	Leu	Gly	Gln	
				725					730					735		
Arg	Ser	Glu	Gln	Ala	Gly	Gly	Leu	Thr	Pro	Gln	Glu	Tyr	Glu	Ile	Ala	
			740					745					750			
Arg	Leu	Val	Ser	Ser	Gly	His	Ala	Asn	Arg	Glu	Val	Ala	Gln	Glu	Leu	
		755						760					765			
Phe	Leu	Ser	Pro	Lys	Thr	Val	Glu	Tyr	His	Leu	Thr	Arg	Val	Tyr	Lys	
	770					775					780					
Lys	Leu	Gly	Ile	Arg	Asn	Arg	Met	Glu	Leu	Ala	Glu	Ala	Leu	Lys	Lys	
785					790					795					800	
Tyr	Ser	His	Asp	Ala												
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 taaaaatccc cgaaacctcc ttggacacat cgcccacaaa ttg ggt gcg cac tcc 115
 Leu Gly Ala His Ser
 1 5
 gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg 163
 Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val
 10 15 20
 gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa 211
 Val Ile Val Ala Asp Val His Trp Ala Asp Val Glu Ser Met Gln Lys
 25 30 35
 ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc 259
 Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly Arg Phe Ala Leu Ile
 40 45 50
 atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc 307
 Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe His Asp Glu Val Val

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tcg	ctc	ccc	tcc	atc	gca	gac	tcc	acc	tac	gta	ttg	ccg	ccg	atg	agt	355
Ser	Leu	Pro	Ser	Ile	Ala	Asp	Ser	Thr	Tyr	Val	Leu	Pro	Pro	Met	Ser	
70					75					80					85	
att	gaa	gaa	atc	cgc	cag	ctt	gcg	ctt	acc	gat	gtc	cgc	ggc	cgc	atc	403
Ile	Glu	Glu	Ile	Arg	Gln	Leu	Ala	Leu	Thr	Asp	Val	Arg	Gly	Arg	Ile	
				90					95					100		
agc	acc	acc	acc	gcc	aca	gac	atc	cag	cgc	atc	acc	ggc	ggc	atc	tac	451
Ser	Thr	Thr	Thr	Ala	Thr	Asp	Ile	Gln	Arg	Ile	Thr	Gly	Gly	Ile	Tyr	
			105					110					115			
ggg	cga	gtc	aaa	gaa	gtc	ctc	cac	tcg	gaa	tcc	ccc	gat	cac	tgg	cga	499
Gly	Arg	Val	Lys	Glu	Val	Leu	His	Ser	Glu	Ser	Pro	Asp	His	Trp	Arg	
		120					125					130				
atg	ccc	aac	cca	aat	att	ccc	atc	cca	caa	agc	tgg	cat	gcc	aac	ctg	547
Met	Pro	Asn	Pro	Asn	Ile	Pro	Ile	Pro	Gln	Ser	Trp	His	Ala	Asn	Leu	
	135					140					145					
ttg	aga	cgc	atc	acc	aac	gaa	gaa	gtc	tgg	cat	gta	cta	ctc	gcc	gtc	595
Leu	Arg	Arg	Ile	Thr	Asn	Glu	Glu	Val	Trp	His	Val	Leu	Leu	Ala	Val	
150					155					160					165	
gct	gtc	ctt	ccc	tcc	gga	ggc	ccc	att	gac	ctg	gta	aaa	ctc	ata	ggc	643
Ala	Val	Leu	Pro	Ser	Gly	Gly	Pro	Ile	Asp	Leu	Val	Lys	Leu	Ile	Gly	
				170					175					180		
aac	gac	ccc	acg	ggc	atg	ctt	tgc	gac	gac	gcc	gtc	cgc	tca	ggc	ctg	691
Asn	Asp	Pro	Thr	Gly	Met	Leu	Cys	Asp	Asp	Ala	Val	Arg	Ser	Gly	Leu	
			185					190					195			
ctc	cgc	gtg	ctg	ccg	tct	gac	ggc	caa	cca	caa	gtg	gat	ttg	gtc	ctg	739
Leu	Arg	Val	Leu	Pro	Ser	Asp	Gly	Gln	Pro	Gln	Val	Asp	Leu	Val	Leu	
		200					205					210				
ccg	atc	gac	cgc	gcc	gta	ctg	caa	tca	cgc	act	ccg	ctc	aac	att	ctg	787
Pro	Ile	Asp	Arg	Ala	Val	Leu	Gln	Ser	Arg	Thr	Pro	Leu	Asn	Ile	Leu	
	215					220					225					
gcg	cag	ttg	cac	cac	aag	gca	gcc	gaa	tat	tac	ggc	aag	tgg	aat	caa	835
Ala	Gln	Leu	His	His	Lys	Ala	Ala	Glu	Tyr	Tyr	Gly	Lys	Trp	Asn	Gln	
230					235					240					245	
aaa	gat	gcc	caa	ctg	gag	cac	gaa	gca	ttt	gct	gca	att	gat	cca	aat	883
Lys	Asp	Ala	Gln	Leu	Glu	His	Glu	Ala	Phe	Ala	Ala	Ile	Asp	Pro	Asn	
				250					255					260		
gat	cca	gca	gtg	cga	gcc	cta	gcg	cag	cgc	gga	tat	gcg	ttg	ggg	agg	931
Asp	Pro	Ala	Val	Arg	Ala	Leu	Ala	Gln	Arg	Gly	Tyr	Ala	Leu	Gly	Arg	
			265					270					275			
act	ggc	cac	tgg	atg	gaa	tcg	gca	cac	gcc	cta	tct	ctt	gcc	gcg	aac	979
Thr	Gly	His	Trp	Met	Glu	Ser	Ala	His	Ala	Leu	Ser	Leu	Ala	Ala	Asn	
		280					285					290				
cgc	act	gca	cac	caa	gaa	gaa	tca	aat	aag	tac	ttg	ctg	gag	tcc	atc	1027
Arg	Thr	Ala	His	Gln	Glu	Glu	Ser	Asn	Lys	Tyr	Leu	Leu	Glu	Ser	Ile	
	295					300					305					

gat tca ctg atc gcc gcc gcc gat ctc ccc caa gct cga tcc aga gca	1075
Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln Ala Arg Ser Arg Ala	
310 315 320 325	
tcc acc ctt gat ctt gga gaa acc ggc att caa caa gac tca atg ctg	1123
Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln Gln Asp Ser Met Leu	
330 335 340	
ggc tac ctg gca atc cac gaa ggc cgg cgc ctc gaa gca cgc aat ctc	1171
Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu Glu Ala Arg Asn Leu	
345 350 355	
ctt cat cgt gct tct gaa gaa ttg ctg gcg cag cac ccg att gat ccg	1219
Leu His Arg Ala Ser Glu Glu Leu Ala Gln His Pro Ile Asp Pro	
360 365 370	
atc cac ggc ccc cgc atg gct cag cgc aaa gta ctg tta aac tta gtg	1267
Ile His Gly Pro Arg Met Ala Gln Arg Lys Val Leu Leu Asn Leu Val	
375 380 385	
gac tgg aat cca gaa gaa ctc ctg gtg tgg gct gat aga gca gtc gca	1315
Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala Asp Arg Ala Val Ala	
390 395 400 405	
tgg act gaa gag gat gct ggc gaa aag gtt gag gcc caa gct att tcc	1363
Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu Ala Gln Ala Ile Ser	
410 415 420	
ctc att gga caa tcc atc ctc gat ggc tgc ctc ccc gaa gat aaa ccc	1411
Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu Pro Glu Asp Lys Pro	
425 430 435	
atc ccc ggt gaa acc acc ctt cac gca caa cgc cgc cac atg gca atg	1459
Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg Arg His Met Ala Met	
440 445 450	
ggc tgg ctt tcc atg gtt cac gat gat cca gta act gca cgt caa aag	1507
Gly Trp Leu Ser Met Val His Asp Asp Pro Val Thr Ala Arg Gln Lys	
455 460 465	
ctt gaa cgt cgc aca tcc atc aat ggt tca gaa cgc atc agt ttg tgg	1555
Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu Arg Ile Ser Leu Trp	
470 475 480 485	
caa gac gga tgg ctg gct cgg tcc cta ctg ctg ctc ggc gaa tgg gag	1603
Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu Leu Gly Glu Trp Glu	
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tcc gca gca cgc acc gta gaa atc ggt ctg gcc cgc gcc gaa cag ttt	1651
Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala Arg Ala Glu Gln Phe	
505 510 515	
ggc atc cgc ttc ctc gaa cca ctg tta ctg tgg tcg ggc gcc aca att	1699
Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp Ser Gly Ala Thr Ile	
520 525 530	
gca aca gcc cgc gga aac tct gac ttg gca cga aat tac atg agc aga	1747
Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg Asn Tyr Met Ser Arg	
535 540 545	

ctg tcc acc gat caa gac tcc ttc atc gtc caa tct atg cca tct gcg	1795
Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln Ser Met Pro Ser Ala	
550 555 560 565	
atg tgt cgc atg tgg gtc cac cgc cat aga aat gaa atc ccc ggt gcg	1843
Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala	
570 575 580	
atc gtg gcc gga gaa caa ttg gaa aaa atc gcc gca cac aaa cac gtc	1891
Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val	
585 590 595	
aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc	1939
Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu	
600 605 610	
atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg	1987
Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Leu Val Asn Ser Thr	
615 620 625	
ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att	2035
Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile	
630 635 640 645	
gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag	2083
Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys	
650 655 660	
gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc	2131
Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr	
665 670 675	
ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg	2179
Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu	
680 685 690	
aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca	2227
Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala	
695 700 705	
gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc	2275
Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala	
710 715 720 725	
aac cga gaa cgc cgg gtg ggt ggc ctt ggt caa cga tcc gag caa gcc	2323
Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala	
730 735 740	
ggt ggg ctc acc cct cag gaa tat gaa att gcc cga tta gtg tca tct	2371
Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala Arg Leu Val Ser Ser	
745 750 755	
ggg cat gcc aac cga gag gtc gca cag gag ctt ttc ctc tcg cct aag	2419
Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu Phe Leu Ser Pro Lys	
760 765 770	
acc gtg gaa tac	2431
Thr Val Glu Tyr	
775	

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<211> 777

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 144

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Asp Ala Ser Thr Val Val Ile Val Ala Asp Val His Trp Ala Asp Val
 20 25 30

Glu Ser Met Gln Lys Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly
 35 40 45

Arg Phe Ala Leu Ile Met Ile Gly Leu Asp Glu Glu Asn Leu Val Phe
 50 55 60

His Asp Glu Val Val Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val
 65 70 75 80

Leu Pro Pro Met Ser Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp
 85 90 95

Val Arg Gly Arg Ile Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile
 100 105 110

Thr Gly Gly Ile Tyr Gly Arg Val Lys Glu Val Leu His Ser Glu Ser
 115 120 125

Pro Asp His Trp Arg Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser
 130 135 140

Trp His Ala Asn Leu Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His
 145 150 155 160

Val Leu Leu Ala Val Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu
 165 170 175

Val Lys Leu Ile Gly Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala
 180 185 190

Val Arg Ser Gly Leu Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln
 195 200 205

Val Asp Leu Val Leu Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr
 210 215 220

Pro Leu Asn Ile Leu Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr
 225 230 235 240

Gly Lys Trp Asn Gln Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala
 245 250 255

Ala Ile Asp Pro Asn Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly
 260 265 270

Tyr Ala Leu Gly Arg Thr Gly His Trp Met Glu Ser Ala His Ala Leu
 275 280 285

Ser Leu Ala Ala Asn Arg Thr Ala His Gln Glu Glu Ser Asn Lys Tyr

290	295	300
Leu 305	Leu 310	Ala 315
Ala 325	Arg 325	Leu 330
Gln 340	Asp 340	Arg 350
Glu 355	Ala 360	Leu 365
His 370	Pro 375	Ala 380
Leu 385	Asn 390	Glu 395
Asp 405	Ala 405	Glu 410
Ala 420	Ile 425	Gln 430
Pro 435	Gly 440	Thr 445
Arg 450	Met 455	His 460
Thr 465	Ala 470	Arg 475
Arg 485	Gln 490	Ala 495
Leu 500	Glu 505	Ile 510
Arg 515	Gly 520	Leu 525
Ser 530	Ala 535	Asn 540
Asn 545	Leu 550	Asp 555
Ser 565	Cys 570	His 575
Glu 580	Ala 585	Lys 590
Ala 595	Pro 600	Trp 605
His 610	Arg 615	Glu 620

Leu Val Asn Ser Thr Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser
 625 630 635 640
 Ala His Ala Lys Ile Ala Val Pro Asp Ala Met Leu Met Ile His His
 645 650 655
 Gly Asp Val Lys Lys Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met
 660 665 670
 Ile Asp Pro Leu Thr Leu Pro Tyr Tyr Arg Ala Arg Ile Cys Phe Glu
 675 680 685
 Tyr Gly Gln Ala Leu Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu
 690 695 700
 Gln Phe Ala Arg Ala Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala
 705 710 715 720
 Met Val Thr Leu Ala Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln
 725 730 735
 Arg Ser Glu Gln Ala Gly Gly Leu Thr Pro Gln Glu Tyr Glu Ile Ala
 740 745 750
 Arg Leu Val Ser Ser Gly His Ala Asn Arg Glu Val Ala Gln Glu Leu
 755 760 765
 Phe Leu Ser Pro Lys Thr Val Glu Tyr
 770 775

<210> 145
 <211> 471
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(448)
 <223> RXA00593

<400> 145
 ttggtgtgat gcattcgaca gcaaattggc tgtgtgacta cacttgcgag tgtattaagt 60
 attaggccgt gcatatgtag cgcatttttaa ggagattgtc atg acg tct gtg att 115
 Met Thr Ser Val Ile
 1 5
 cca gag cag cgc aac aac ccc ttt tat agg gac agc gcc aca att gct 163
 Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp Ser Ala Thr Ile Ala
 10 15 20
 tcc tcg gac cac aca gag cgt ggt gag tgg gtc act cag gca aag tgt 211
 Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val Thr Gln Ala Lys Cys
 25 30 35
 cga aat ggc gac cca gat gca ttg ttt gtt cgt ggt gca gcg caa cgc 259
 Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg Gly Ala Ala Gln Arg
 40 45 50

cga gca gca gca att tgc cgc cac tgc cct gta gcc atg cag tgc tgc 307
 Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val Ala Met Gln Cys Cys
 55 60 65

gcc gat gcc tta gat aac aag gtg gaa ttc gga gtc tgg gga ggc ctg 355
 Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly Val Trp Gly Gly Leu
 70 75 80 85

acc gag cgc cag cgc cgt gca ttg ctt cga aag aag ccg cac att act 403
 Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys Lys Pro His Ile Thr
 90 95 100

aac tgg gct gaa tat ttg gct cag ggg ggc gag atc gcc ggg gtt 448
 Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu Ile Ala Gly Val
 105 110 115

taattaattt caagggctgg cca 471

<210> 146

<211> 116

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

Met Thr Ser Val Ile Pro Glu Gln Arg Asn Asn Pro Phe Tyr Arg Asp
 1 5 10 15

Ser Ala Thr Ile Ala Ser Ser Asp His Thr Glu Arg Gly Glu Trp Val
 20 25 30

Thr Gln Ala Lys Cys Arg Asn Gly Asp Pro Asp Ala Leu Phe Val Arg
 35 40 45

Gly Ala Ala Gln Arg Arg Ala Ala Ala Ile Cys Arg His Cys Pro Val
 50 55 60

Ala Met Gln Cys Cys Ala Asp Ala Leu Asp Asn Lys Val Glu Phe Gly
 65 70 75 80

Val Trp Gly Gly Leu Thr Glu Arg Gln Arg Arg Ala Leu Leu Arg Lys
 85 90 95

Lys Pro His Ile Thr Asn Trp Ala Glu Tyr Leu Ala Gln Gly Gly Glu
 100 105 110

Ile Ala Gly Val
 115

<210> 147

<211> 967

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXA02724

<400> 147

cgagcgcgca cgcggtggcc accgccaagc tcattgcgga tccggactcc gatttcatgg 60

ctgatctgga ggaagcgcgg cgcgtggata atatgggtgc atg ctg atc ggt gag 115
Met Leu Ile Gly Glu
1 5

gtg tcc aag ctc agt ggg gtg agt gcg cgc atg ttg cgg cac tac gaa 163
Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met Leu Arg His Tyr Glu
10 15 20

aag ctg ggt ttg gtc gag ccg aag cag tgc acg gcg ggg tat cgg gaa 211
Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr Ala Gly Tyr Arg Glu
25 30 35

tac tca gaa ggc gat gtg cgc agg att ttc cat atc gaa ggt ttg cgc 259
Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His Ile Glu Gly Leu Arg
40 45 50

agc ttg ggt ctt agt ttg aag cag gtt gga gac gcg ctt gag gat cca 307
Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp Ala Leu Glu Asp Pro
55 60 65

gac ttt gat cct cag gca gtc att tcc gag atg att gct gag act tct 355
Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met Ile Ala Glu Thr Ser
70 75 80 85

gcg cgg att tct atg gaa cgg gag ttg ctt gcc agg ctg aaa gcg gtg 403
Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala Arg Leu Lys Ala Val
90 95 100

cgt cat gcg cag gcc tgc gat tgg gaa tgc gcg ttg gat gcg gtg cag 451
Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala Leu Asp Ala Val Gln
105 110 115

att tta cgt cgc ctg cga tgc ggg gat ccg gcg caa cgt caa gcc gtg 499
Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala Gln Arg Gln Ala Val
120 125 130

gcc tat gac tct gtc tct ggt aaa gaa gca gtt gcg cta gaa acc ttg 547
Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val Ala Leu Glu Thr Leu
135 140 145

gtg gaa tgc gcg ctc ggt gag tgc cat ttg aac gcg gag ggg gcg ctg 595
Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn Ala Glu Gly Ala Leu
150 155 160 165

tgc tgg gcg gtt gtg cag cgt ggt gag gaa gct gtt gca ttg gcg gca 643
Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala Val Ala Leu Ala Ala
170 175 180

cga ggt ttg cgc tca agg gat gcg gcg gtg cgg ctg cgg gct gta agg 691
Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg Leu Arg Ala Val Arg
185 190 195

att gtg gcg agc gcg ccg agt gct gtt gcg gat cga gta gag tgg cta 739
Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp Arg Val Glu Trp Leu
200 205 210

cgg cca atg att cgc gat ccc gat gct ctc gtg cgt gct gaa act gcg 787
Arg Pro Met Ile Arg Asp Pro Asp Ala Leu Val Arg Ala Glu Thr Ala
215 220 225

ttg gcg ttg gga aaa tca ggc gat gag agt gca gtt gag cag ctc gtg 835
 Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala Val Glu Gln Leu Val
 230 235 240 245

tcc atg gtt ctc acc ggt ctt cgg gac gtg gag gca gcc gaa ttg ctt 883
 Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu Ala Ala Glu Leu Leu
 250 255 260

gcc gga ttt ggg gag ccc gtg cag tta gat gtg ttc aag aaa ttt gcg 931
 Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val Phe Lys Lys Phe Ala
 265 270 275

cgg acg ctg gat gat gag gaa aca atg tcc ccg acg 967
 Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro Thr
 280 285

<210> 148

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

Met Leu Ile Gly Glu Val Ser Lys Leu Ser Gly Val Ser Ala Arg Met
 1 5 10 15

Leu Arg His Tyr Glu Lys Leu Gly Leu Val Glu Pro Lys Gln Ser Thr
 20 25 30

Ala Gly Tyr Arg Glu Tyr Ser Glu Gly Asp Val Arg Arg Ile Phe His
 35 40 45

Ile Glu Gly Leu Arg Ser Leu Gly Leu Ser Leu Lys Gln Val Gly Asp
 50 55 60

Ala Leu Glu Asp Pro Asp Phe Asp Pro Gln Ala Val Ile Ser Glu Met
 65 70 75 80

Ile Ala Glu Thr Ser Ala Arg Ile Ser Met Glu Arg Glu Leu Leu Ala
 85 90 95

Arg Leu Lys Ala Val Arg His Ala Gln Ala Ser Asp Trp Glu Ser Ala
 100 105 110

Leu Asp Ala Val Gln Ile Leu Arg Arg Leu Arg Ser Gly Asp Pro Ala
 115 120 125

Gln Arg Gln Ala Val Ala Tyr Asp Ser Val Ser Gly Lys Glu Ala Val
 130 135 140

Ala Leu Glu Thr Leu Val Glu Ser Ala Leu Gly Glu Ser His Leu Asn
 145 150 155 160

Ala Glu Gly Ala Leu Ser Trp Ala Val Val Gln Arg Gly Glu Glu Ala
 165 170 175

Val Ala Leu Ala Ala Arg Gly Leu Arg Ser Arg Asp Ala Ala Val Arg
 180 185 190

Leu Arg Ala Val Arg Ile Val Ala Ser Ala Pro Ser Ala Val Ala Asp

195	200	205
Arg Val Glu Trp Leu Arg 210	Pro Met Ile Arg Asp 215	Pro Asp Ala Leu Val 220
Arg Ala Glu Thr Ala Leu Ala Leu Gly Lys Ser Gly Asp Glu Ser Ala 225	230	235 240
Val Glu Gln Leu Val Ser Met Val Leu Thr Gly Leu Arg Asp Val Glu 245	250	255
Ala Ala Glu Leu Leu Ala Gly Phe Gly Glu Pro Val Gln Leu Asp Val 260	265	270
Phe Lys Lys Phe Ala Arg Thr Leu Asp Asp Glu Glu Thr Met Ser Pro 275	280	285

Thr

<210> 149
 <211> 420
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(397)
 <223> RXA00494

<400> 149
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 aaagctataa aaagtagctg acaataggga gtatttgaag atg aca ttg cct cac 115
 Met Thr Leu Pro His
 1 5
 cag ctt ccc ggg cca aat gca gac ttc tgg gac tgg cag ttg cac gga 163
 Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp Trp Gln Leu His Gly
 10 15 20
 acg tgc cgc ggc gag acc tcc gac gtg ttc tat cac ccg gac ggc gag 211
 Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr His Pro Asp Gly Glu
 25 30 35
 cgc ggt cgt gct cgc cag cgt cgg gag ctg cgc gca aag gcc atc tgt 259
 Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg Ala Lys Ala Ile Cys
 40 45 50
 gca gca tgc cca gta ttg gaa tcc tgc cgc aag cat gca cta gct gta 307
 Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys His Ala Leu Ala Val
 55 60 65
 gca gag cct tat gga gta tgg ggc gga ctt tca gag tcc gaa cga ctg 355
 Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser Glu Ser Glu Arg Leu
 70 75 80 85
 gtt atc ctt cgc aac aac gag cgc aag caa cca gta gca gtt 397
 Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro Val Ala Val
 90 95

taaaagagca gacccggtca cca

420

<210> 150

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Met Thr Leu Pro His Gln Leu Pro Gly Pro Asn Ala Asp Phe Trp Asp
1 5 10 15

Trp Gln Leu His Gly Thr Cys Arg Gly Glu Thr Ser Asp Val Phe Tyr
20 25 30

His Pro Asp Gly Glu Arg Gly Arg Ala Arg Gln Arg Arg Glu Leu Arg
35 40 45

Ala Lys Ala Ile Cys Ala Ala Cys Pro Val Leu Glu Ser Cys Arg Lys
50 55 60

His Ala Leu Ala Val Ala Glu Pro Tyr Gly Val Trp Gly Gly Leu Ser
65 70 75 80

Glu Ser Glu Arg Leu Val Ile Leu Arg Asn Asn Glu Arg Lys Gln Pro
85 90 95

Val Ala Val

<210> 151

<211> 435

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> RXN01368

<400> 151

tcgcttgga gaaggaaaaa ttttccaaac ctgctcgagg accaacaatcc ccgatgagaa 60

cagacttaaa gtagctttga aagtgagagg ggggagagta atg gaa gat tca gct 115
Met Glu Asp Ser Ala
1 5

ggg gac gta tct gca aag ttg aaa gca ggc cag act cgc acc gca ctg 163
Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln Thr Arg Thr Ala Leu
10 15 20

gag atg act ttg gat gat ctg ttc gga gcg gtt gag caa gaa tgg cag 211
Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val Glu Gln Glu Trp Gln
25 30 35

gag cag gcg ctg tgt gcg caa act gat cct gaa gca ttc ttt cca gaa 259
Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe Phe Pro Glu
40 45 50

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aaa ggt ggc tca act cgc gaa gcc aag cgg atc tgc cag ggc tgc ccg 307
Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Gln Gly Cys Pro
    55                60                65

ggt cgg gat gaa tgc cta gag ttt gct ctt gag cat gat gaa cgc ttt 355
Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu His Asp Glu Arg Phe
    70                75                80                85

gga att tgg ggt ggt ctc tct gaa cgt gag cgc cgc cgc ctg aaa cgc 403
Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg Arg Arg Leu Lys Arg
                90                95                100

gaa att tcg taaaacttca agaccagtaa gcg 435
Glu Ile Ser

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<210> 152
<211> 104
<212> PRT
<213> Corynebacterium glutamicum

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<400> 152
Met Glu Asp Ser Ala Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln
  1                5                10                15

Thr Arg Thr Ala Leu Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val
                20                25                30

Glu Gln Glu Trp Gln Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu
                35                40                45

Ala Phe Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile
    50                55                60

Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu
    65                70                75                80

His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg
                85                90                95

Arg Arg Leu Lys Arg Glu Ile Ser
    100

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<210> 153
<211> 152
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(129)
<223> FRXA01368

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<400> 153
aag cgg atc tgc cag ggc tgc ccg gtt cgg gat gaa tgc cta gag ttt 48
Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
  1                5                10                15

gct ctt gag cat gat gaa cgc ttt gga att tgg ggt ggt ctc tct gaa 96

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Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
 20 25 30

cgt gag cgc cgc cgc ctg aaa cgc gaa att tcg taaaacttca agaccagtaa 149
 Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
 35 40

gcg 152

<210> 154
 <211> 43
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 154
 Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
 1 5 10 15

Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
 20 25 30

Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
 35 40

<210> 155
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXN00464

<400> 155
 gaataaacca aagggtggac acttattcga acgggtgctt gatttaggca acttgagcaa 60

aattctgcca tttcgctca aatcgggcta gttttgaagc atg agc gaa cgt cag 115
 Met Ser Glu Arg Gln
 1 5

ctg gaa aag tca att gag cac gcc gtc gag tta gcc cgc gaa gcc cga 163
 Leu Glu Lys Ser Ile Glu His Ala Val Glu Leu Ala Arg Glu Ala Arg
 10 15 20

aac atc gaa gtt ttt acc gga gcc gga atg agc gcc gac tcc ggg ttg 211
 Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser Ala Asp Ser Gly Leu
 25 30 35

gaa acg tat cgt gat gat aaa acc ggg ctg tgg agc aac gta gat cca 259
 Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp Ser Asn Val Asp Pro
 40 45 50

caa gcg atg gca agt atc gat gca tgg cgc aaa gat cca gag cca atg 307
 Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys Asp Pro Glu Pro Met
 55 60 65

tgg gcg tgg tat cgc tgg cgc gcc ggg gtg gca gct agg gca gaa ccc 355
 Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala Ala Arg Ala Glu Pro

70	75	80	85	
aac gcg ggg cat	caa gct att tcc tac tgg	gag ggg agt gac acc gtc	403	
Asn Ala Gly His	Gln Ala Ile Ser Tyr Trp	Glu Gly Ser Asp Thr Val		
	90	95 100		
gaa cac gtt cac	atc acc acc cag aac att gac	aac ctg cac gag cga	451	
Glu His Val His	Ile Thr Thr Gln Asn Ile Asp	Asn Leu His Glu Arg		
	105	110 115		
gct ggc tct agc	gat gtg aca cat ctt cat ggc	agc ttg ttt gaa tac	499	
Ala Gly Ser Ser	Asp Val Thr His Leu His Gly	Ser Leu Phe Glu Tyr		
	120	125 130		
agg tgc tct gat	tgt gcg act cca tgg gaa gac	gat aaa aac tat ccg	547	
Arg Cys Ser Asp	Cys Ala Thr Pro Trp Glu Asp	Asp Lys Asn Tyr Pro		
	135	140 145		
caa gaa ccc att	gca cgc ctt gct cct cca caa	tgt gaa aag tgc gga	595	
Gln Glu Pro Ile	Ala Arg Leu Ala Pro Pro Gln	Cys Glu Lys Cys Gly		
	150	155 160 165		
ggg ctg att aga	cca ggt gtg gtg tgg ttt ggt	gag aac ctg ccc gta	643	
Gly Leu Ile Arg	Pro Gly Val Val Trp Phe Gly	Glu Asn Leu Pro Val		
	170	175 180		
gaa gag tgg gat	att gca gag caa cgc atc gca	gaa gcc gat ctc atg	691	
Glu Glu Trp Asp	Ile Ala Glu Gln Arg Ile Ala	Glu Ala Asp Leu Met		
	185	190 195		
atc att gtg ggt	acc tcc ggg att gtt cat cct	gca gca gca ctc ccg	739	
Ile Ile Val Gly	Thr Ser Gly Ile Val His Pro	Ala Ala Ala Leu Pro		
	200	205 210		
caa tta gcc caa	caa cgc ggc gtt ccc atc gtg	gag atc tcc cca acg	787	
Gln Leu Ala Gln	Gln Arg Gly Val Pro Ile Val	Glu Ile Ser Pro Thr		
	215	220 225		
cgc acc gaa ctt	agc cgg atc goa gac ttc acc	tgg atg tcc acc gca	835	
Arg Thr Glu Leu	Ser Arg Ile Ala Asp Phe Thr	Trp Met Ser Thr Ala		
	230	235 240 245		
gcc caa gcg cta	cca gcg ttg atg cga ggt ttg	agc gcc taacatgact	884	
Ala Gln Ala Leu	Pro Ala Leu Met Arg Gly Leu	Ser Ala		
	250	255		
gaagatgact tag			897	
<210> 156				
<211> 258				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 156				
Met Ser Glu Arg	Gln Leu Glu Lys Ser Ile Glu	His Ala Val Glu Leu		
1	5	10	15	
Ala Arg Glu Ala	Arg Asn Ile Glu Val Phe Thr	Gly Ala Gly Met Ser		
	20	25 30		

Ala Asp Ser Gly Leu Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp
 35 40 45

Ser Asn Val Asp Pro Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys
 50 55 60

Asp Pro Glu Pro Met Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala
 65 70 75 80

Ala Arg Ala Glu Pro Asn Ala Gly His Gln Ala Ile Ser Tyr Trp Glu
 85 90 95

Gly Ser Asp Thr Val Glu His Val His Ile Thr Thr Gln Asn Ile Asp
 100 105 110

Asn Leu His Glu Arg Ala Gly Ser Ser Asp Val Thr His Leu His Gly
 115 120 125

Ser Leu Phe Glu Tyr Arg Cys Ser Asp Cys Ala Thr Pro Trp Glu Asp
 130 135 140

Asp Lys Asn Tyr Pro Gln Glu Pro Ile Ala Arg Leu Ala Pro Pro Gln
 145 150 155 160

Cys Glu Lys Cys Gly Gly Leu Ile Arg Pro Gly Val Val Trp Phe Gly
 165 170 175

Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu Gln Arg Ile Ala
 180 185 190

Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly Ile Val His Pro
 195 200 205

Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val
 210 215 220

Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr
 225 230 235 240

Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu
 245 250 255

Ser Ala

<210> 157
 <211> 355
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (75)..(332)
 <223> FRXA00464

<400> 157
 atccgcaaga acccattgca cgccttgctc ctccacaatg tgaaaagtgc ggagggctga 60

ttagaccagg tgtg gtg tgg ttt ggt gag aac ctg ccc gta gaa gag tgg 110
 Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp

	1	5	10	
gat att gca gag caa cgc atc gca gaa gcc gat ctc atg atc att gtg				158
Asp Ile Ala Glu Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val	15	20	25	
ggt acc tcc ggg att gtt cat cct gca gca gca ctc ccg caa tta gcc				206
Gly Thr Ser Gly Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala	30	35	40	
caa caa cgc ggc gtt ccc atc gtg gag atc tcc cca acg cgc acc gaa				254
Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu	45	50	55	60
ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca gcc caa gcg				302
Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala	65	70	75	
cta cca gcg ttg atg cga ggt ttg agc gcc taacatgact gaagatgact tag				355
Leu Pro Ala Leu Met Arg Gly Leu Ser Ala	80	85		

<210> 158
 <211> 86
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
 Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu
 1 5 10 15
 Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly
 20 25 30
 Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly
 35 40 45
 Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile
 50 55 60
 Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu
 65 70 75 80
 Met Arg Gly Leu Ser Ala
 85

<210> 159
 <211> 1482
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1459)
 <223> RXA01655

<400> 159
 gtttcggtca tgacagatga tccaacgccca caaagtggac tagcggtaga tccactttca 60

gtcacttgca ttagaccact tttttgagga cgatgaagcc	atg ctt gcc gac ctt	115
	Met Leu Ala Asp Leu	
	1 5	
ccc atc gcc tta aac cca cac gaa cca aca tcc atc ccc acg cag ctc	163	
Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser Ile Pro Thr Gln Leu		
	10 15 20	
aca gaa cag atc cgt cgt ctc gtg gcg agg gga att ctc acc cca gga	211	
Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly Ile Leu Thr Pro Gly		
	25 30 35	
gac ccg ctt ccc agc agt cgc tca cta tcc acc caa ttg ggg gta tcc	259	
Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr Gln Leu Gly Val Ser		
	40 45 50	
cgc ggc agt gtg gtg acc gct tat gac caa ttg gcc ggt gaa ggc tac	307	
Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu Ala Gly Glu Gly Tyr		
	55 60 65	
ctc agc acc gcc cgc ggt tcc ggt aca acg atc aac cca gat ctg cat	355	
Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile Asn Pro Asp Leu His		
	70 75 80 85	
ttg ttg aag cct gtg gaa att gag aag aag gag acg tcg aga agc gtc	403	
Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu Thr Ser Arg Ser Val		
	90 95 100	
ccg ccc ccg ctg ctc aac ctg agc ccc ggc gtg ccc gat acc gcg acg	451	
Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val Pro Asp Thr Ala Thr		
	105 110 115	
ctc gcc gat tcc gca tgg cgc gct gcg tgg cgc gaa gcc tgc gcc aag	499	
Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg Glu Ala Cys Ala Lys		
	120 125 130	
cca ccc acg cac tcc cct gag cag gga ctt ttg agg ctg cgg atc gag	547	
Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu Arg Leu Arg Ile Glu		
	135 140 145	
atc gcc gac cac ctg cgc cag atg cgt ggc ctc atg gtc gag ccg gag	595	
Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu Met Val Glu Pro Glu		
	150 155 160 165	
cag atc atc gtc acc gcc ggc gcg cgc gag ggg ctg agt ctg ctg ctg	643	
Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly Leu Ser Leu Leu Leu		
	170 175 180	
cgc acc atg gat gcg cct gcc cgc atc ggc gtc gaa tcg ccc ggc tac	691	
Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val Glu Ser Pro Gly Tyr		
	185 190 195	
ccc agc ctg cgc cgc atc ccg cag gtg ctt ggc cat gag acg atc gat	739	
Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly His Glu Thr Ile Asp		
	200 205 210	
gtg ccg acc gac gaa tcc ggc ctc gta ccc cgc gcg ctg ccc cac gac	787	
Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg Ala Leu Pro His Asp		
	215 220 225	
ctt aac gcg cta ctg gta acc cct agc cat caa tat ccc tac ggc ggc	835	

Leu	Asn	Ala	Leu	Leu	Val	Thr	Pro	Ser	His	Gln	Tyr	Pro	Tyr	Gly	Gly		
230					235					240					245		
tcg	ctg	ccc	gcc	gat	cgc	cgc	acc	gcg	cta	gtc	gcg	tgg	gct	gag	gca		883
Ser	Leu	Pro	Ala	Asp	Arg	Arg	Thr	Ala	Leu	Val	Ala	Trp	Ala	Glu	Ala		
				250					255					260			
aac	gat	gcg	ttg	ctt	att	gaa	gac	gac	ttc	gat	tct	gag	ctg	cgc	tac		931
Asn	Asp	Ala	Leu	Leu	Ile	Glu	Asp	Asp	Phe	Asp	Ser	Glu	Leu	Arg	Tyr		
			265					270					275				
gtc	ggt	atg	ccg	ctt	ccg	ccg	ctg	cgt	gcg	ctg	gcg	ccc	gat	cgc	acg		979
Val	Gly	Met	Pro	Leu	Pro	Pro	Leu	Arg	Ala	Leu	Ala	Pro	Asp	Arg	Thr		
		280					285					290					
att	ctg	ctc	ggc	acg	ttt	tcc	tcc	gtg	atc	aca	cca	caa	gtc	gcc	tgc		1027
Ile	Leu	Leu	Gly	Thr	Phe	Ser	Ser	Val	Ile	Thr	Pro	Gln	Val	Ala	Cys		
	295					300					305						
gga	tac	ctc	atc	gcg	ccg	acg	ccc	cag	gcg	cgc	gtg	ctc	gcc	acg	ctt		1075
Gly	Tyr	Leu	Ile	Ala	Pro	Thr	Pro	Gln	Ala	Arg	Val	Leu	Ala	Thr	Leu		
310					315					320					325		
cgc	ggg	att	ctc	ggc	cag	cca	gtc	ggc	gcc	atc	acc	caa	cac	gcg	ctc		1123
Arg	Gly	Ile	Leu	Gly	Gln	Pro	Val	Gly	Ala	Ile	Thr	Gln	His	Ala	Leu		
				330					335					340			
gcg	tcc	tac	ctc	gcc	tca	ggc	gct	tta	cga	cgc	cgc	acc	caa	cgt	ttg		1171
Ala	Ser	Tyr	Leu	Ala	Ser	Gly	Ala	Leu	Arg	Arg	Arg	Thr	Gln	Arg	Leu		
			345				350						355				
cgg	cgc	ctt	tac	cga	cac	cgc	cgc	tcc	atc	gtc	caa	gac	acc	ctc	ggt		1219
Arg	Arg	Leu	Tyr	Arg	His	Arg	Arg	Ser	Ile	Val	Gln	Asp	Thr	Leu	Gly		
		360					365					370					
gac	ctc	ccg	aat	acg	cag	ctt	cgc	ccc	atc	aac	ggt	ggc	ctc	cac	gca		1267
Asp	Leu	Pro	Asn	Thr	Gln	Leu	Arg	Pro	Ile	Asn	Gly	Gly	Leu	His	Ala		
	375					380					385						
gtt	ctc	ctt	tgc	gac	aaa	ccc	caa	gac	ctc	gtt	gtc	acc	aca	ctc	gcc		1315
Val	Leu	Leu	Cys	Asp	Lys	Pro	Gln	Asp	Leu	Val	Val	Thr	Thr	Leu	Ala		
390					395					400					405		
tcc	cga	ggc	ctt	aac	gtc	acc	gcg	ctt	tcc	cac	tac	tgg	ggc	ggc	acc		1363
Ser	Arg	Gly	Leu	Asn	Val	Thr	Ala	Leu	Ser	His	Tyr	Trp	Gly	Gly	Thr		
				410					415					420			
ggc	gca	gac	aac	ggc	atc	gtc	ttc	ggc	ttc	ggc	tcc	cac	gac	gaa	gac		1411
Gly	Ala	Asp	Asn	Gly	Ile	Val	Phe	Gly	Phe	Gly	Ser	His	Asp	Glu	Asp		
			425					430					435				
acc	ctc	aga	tgg	gtg	ctt	gct	gag	atc	agc	gat	gcg	gtg	tct	cta	ggc		1459
Thr	Leu	Arg	Trp	Val	Leu	Ala	Glu	Ile	Ser	Asp	Ala	Val	Ser	Leu	Gly		
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<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

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Ile Leu Thr Pro Gly Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr
          35           40           45

Gln Leu Gly Val Ser Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu
 50           55           60

Ala Gly Glu Gly Tyr Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile
 65           70           75           80

Asn Pro Asp Leu His Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu
          85           90           95

Thr Ser Arg Ser Val Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val
          100          105          110

Pro Asp Thr Ala Thr Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg
          115          120          125

Glu Ala Cys Ala Lys Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu
          130          135          140

Arg Leu Arg Ile Glu Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu
          145          150          155          160

Met Val Glu Pro Glu Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly
          165          170          175

Leu Ser Leu Leu Leu Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val
          180          185          190

Glu Ser Pro Gly Tyr Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly
          195          200          205

His Glu Thr Ile Asp Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg
          210          215          220

Ala Leu Pro His Asp Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln
          225          230          235          240

Tyr Pro Tyr Gly Gly Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val
          245          250          255

Ala Trp Ala Glu Ala Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp
          260          265          270

Ser Glu Leu Arg Tyr Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu
          275          280          285

Ala Pro Asp Arg Thr Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr
          290          295          300

Pro Gln Val Ala Cys Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg

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acatcaatgc ggtgaccaca attgggagga gaagtagcac																115
Val Thr Thr Pro Ala																5
gag aac aac acc ctt agc ccc gag acc aaa gta agc atc act ggt cga																163
Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val Ser Ile Thr Gly Arg																20
aac gtt gag gtt cct gat cac ttt gca gaa cga gta aat acc aaa ctc																211
Asn Val Glu Val Pro Asp His Phe Ala Glu Arg Val Asn Thr Lys Leu																35
gca aag att gag cgc ctc gac cca acg ctg acc ttc ttc cac gtt gag																259
Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr Phe Phe His Val Glu																40
cta cag cac gag cca aac cca cgt cgt gct gac gaa agt gat cgc att																307
Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp Glu Ser Asp Arg Ile																

55	60	65	
cag atc acc gcc acc ggc aag gga cac atc gcc cga gca gaa gca aag			355
Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala Arg Ala Glu Ala Lys			
70	75	80	85
gaa gac agc ttc tac gcg gca ctg gaa act gca cta gcc aag atg gag			403
Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala Leu Ala Lys Met Glu			
	90	95	100
cgc tcc ctg cgc aaa gtg aag gca cgt cgc agc att tcc cgc tcc ggt			451
Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser Ile Ser Arg Ser Gly			
	105	110	115
cac cgc gca cca cta ggc act ggt gag gtc ggt gca cag ttg gta gcc			499
His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly Ala Gln Leu Val Ala			
	120	125	130
gag tcc caa gag gca cgc ggt gcc gat gaa ctg ggc aaa tac gat gtt			547
Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu Gly Lys Tyr Asp Val			
	135	140	145
gat cct tat gca gat aag gtc gat gac gtc atg cca ggc cag gtt gtt			595
Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met Pro Gly Gln Val Val			
	150	155	160
cgt acc aag gaa cac cca gca acc cca atg agt gtg gat gac gca cta			643
Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser Val Asp Asp Ala Leu			
	170	175	180
tcc gag atg gaa ttg gtt gga cac gat ttc tac ctc ttc gtc aac gaa			691
Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr Leu Phe Val Asn Glu			
	185	190	195
gag acc aac cag cca tcg gtg gtg tac cgc cga cac gca ttc gac tat			739
Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg His Ala Phe Asp Tyr			
	200	205	210
gga tta att tcc ctg tcc gat gca tagcaattag ttgctaagta ccc			786
Gly Leu Ile Ser Leu Ser Asp Ala			
	215	220	
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Ser Ile Thr Gly Arg Asn Val Glu Val Pro Asp His Phe Ala Glu Arg			
	20	25	30
Val Asn Thr Lys Leu Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr			
	35	40	45
Phe Phe His Val Glu Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp			
	50	55	60

Glu Ser Asp Arg Ile Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala
 65 70 75 80
 Arg Ala Glu Ala Lys Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala
 85 90 95
 Leu Ala Lys Met Glu Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser
 100 105 110
 Ile Ser Arg Ser Gly His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly
 115 120 125
 Ala Gln Leu Val Ala Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu
 130 135 140
 Gly Lys Tyr Asp Val Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met
 145 150 155 160
 Pro Gly Gln Val Val Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser
 165 170 175
 Val Asp Asp Ala Leu Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr
 180 185 190
 Leu Phe Val Asn Glu Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg
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 His Ala Phe Asp Tyr Gly Leu Ile Ser Leu Ser Asp Ala
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<210> 163

<211> 678

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(655)

<223> RXN02450

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actgatcaga gcccgtcct caacaagaag agcaacacca atg aat ctg aaa gat 115
 Met Asn Leu Lys Asp
 1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163
 Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu
 10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211
 Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala
 25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259
 Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn
 40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307

Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val
 55 60 65
 cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355
 Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu
 70 75 80 85
 tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403
 Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn
 90 95 100
 gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451
 Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala
 105 110 115
 gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tcg gtg 499
 Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val
 120 125 130
 ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547
 Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser
 135 140 145
 ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595
 Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln
 150 155 160 165
 gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643
 Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu
 170 175 180
 gca gtt ttc caa taggcaatgc gcccgaatcc cct 678
 Ala Val Phe Gln
 185

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 Asp Val Ala His Glu Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser
 20 25 30
 Met Asn Gln Ile Ala Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr
 35 40 45
 Leu His Phe Arg Asn Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu
 50 55 60
 Leu Glu Pro Ala Val Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro
 65 70 75 80
 Glu His Thr Leu Glu Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu
 85 90 95
 Val Trp Lys Ala Asn Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met

100					105					110					
Val	Glu	Asp	Ala	Ala	Val	Ala	Asp	Glu	Trp	Leu	Ser	Met	Met	Gln	Arg
		115					120					125			
Leu	Ser	Gln	Ser	Val	Pro	Glu	Leu	Val	Glu	Asn	Glu	Glu	Arg	Arg	Val
		130					135					140			
Gln	Phe	Leu	Ala	Ser	Leu	Met	Gly	Met	Asp	Arg	Asn	Phe	Tyr	Phe	Leu
							150					155			160
Tyr	Val	Arg	Gly	Gln	Asp	Val	Asp	Glu	Glu	Leu	Leu	Lys	Leu	Ala	Val
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Ala	Arg	Gln	Trp	Leu	Ala	Val	Phe	Gln							
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<223> FRXA02450

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	Met Asn Leu Lys Asp	
	1 5	

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa	163
Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu	
	10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct	211
Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala	
	25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac	259
Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn	
	40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc	307
Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val	
	55 60 65

cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag	355
Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu	
	70 75 80 85

tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat	403
Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn	
	90 95 100

gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg	451
Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala	

105										110					115					
gtg	gcc	gat	gag	tgg	ctt	tca	atg	atg	cag	agg	ttg	agc	caa	tcg	gtg	499				
Val	Ala	Asp	Glu	Trp	Leu	Ser	Met	Met	Gln	Arg	Leu	Ser	Gln	Ser	Val					
		120					125					130								
ccc	gaa	ttg	gtt	gag	aat	gaa	gag	cgt	cga	gtt	cag	ttc	ctg	gct	agc	547				
Pro	Glu	Leu	Val	Glu	Asn	Glu	Glu	Arg	Arg	Val	Gln	Phe	Leu	Ala	Ser					
	135					140					145									
ttg	atg	ggc	atg	gat	aga	aac	ttt	tac	ttc	ctc	tat	gtc	cga	ggg	caa	595				
Leu	Met	Gly	Met	Asp	Arg	Asn	Phe	Tyr	Phe	Leu	Tyr	Val	Arg	Gly	Gln					
150					155					160					165					
gat	gtt	gat	gag	gaa	ttg	cta	aag	ttg	gct	gtg	gct	cgc	caa	tggt	ttg	643				
Asp	Val	Asp	Glu	Glu	Leu	Leu	Lys	Leu	Ala	Val	Ala	Arg	Gln	Trp	Leu					
				170					175					180						
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Ala	Val	Phe	Gln																	
			185																	

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<212> PRT

<213> Corynebacterium glutamicum

<400> 166

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			20					25					30		
Met	Asn	Gln	Ile	Ala	Gln	Ala	Ala	Gly	Gly	Ser	Arg	Ala	Asn	Leu	Tyr
		35					40					45			
Leu	His	Phe	Arg	Asn	Lys	Pro	Asp	Leu	Met	Met	Ala	Lys	Met	Arg	Glu
	50					55					60				
Leu	Glu	Pro	Ala	Val	Arg	Thr	Pro	Val	Leu	Lys	Val	Phe	Asp	Leu	Pro
65					70					75					80
Glu	His	Thr	Leu	Glu	Ser	Ile	Leu	Arg	Trp	Leu	Asp	Ser	Met	Thr	Glu
			85						90					95	
Val	Trp	Lys	Ala	Asn	Ala	Lys	Val	Phe	Gly	Ala	Met	Glu	Gln	Ala	Met
			100					105					110		
Val	Glu	Asp	Ala	Ala	Val	Ala	Asp	Glu	Trp	Leu	Ser	Met	Met	Gln	Arg
	115						120					125			
Leu	Ser	Gln	Ser	Val	Pro	Glu	Leu	Val	Glu	Asn	Glu	Glu	Arg	Arg	Val
	130					135					140				
Gln	Phe	Leu	Ala	Ser	Leu	Met	Gly	Met	Asp	Arg	Asn	Phe	Tyr	Phe	Leu
145					150				155						160
Tyr	Val	Arg	Gly	Gln	Asp	Val	Asp	Glu	Glu	Leu	Leu	Lys	Leu	Ala	Val
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180 185

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<222> (101)..(793)
<223> RXA01898

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Met Ser Val Lys Ala
1 5
cat gaa tct gtc atg gat tgg gtc acc gag gag ctc cgc agc ggt cgc 163
His Glu Ser Val Met Asp Trp Val Thr Glu Glu Leu Arg Ser Gly Arg
10 15 20
cta aaa atc ggt gac cac ctc ccc agc gaa cgg gcg ctc tcc gaa acc 211
Leu Lys Ile Gly Asp His Leu Pro Ser Glu Arg Ala Leu Ser Glu Thr
25 30 35
ctc gga gtt tcc cga agc tcc ctg cgc gag gcg ctt cgt gtg ctc gaa 259
Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala Leu Arg Val Leu Glu
40 45 50
gcc ctc ggc acc att tcc acc gcc acc gga tcc ggc ccg cgg tct ggc 307
Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser Gly Pro Arg Ser Gly
55 60 65
acc atc atc act gct gcc cct ggc cag gcg ctt tcc ctc tcc gtg acg 355
Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu Ser Leu Ser Val Thr
70 75 80 85
ctg cag ttg gtc acc aac cag gtc ggc cac cac gat att tat gaa acc 403
Leu Gln Leu Val Thr Asn Gln Val Gly His His Asp Ile Tyr Glu Thr
90 95 100
cgc caa ctc ctt gaa ggc tgg gct gcc ctg cat tcc agc gcc gaa cgt 451
Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His Ser Ser Ala Glu Arg
105 110 115
ggc gac tgg gac gtg gca gaa gcg ttg ctg gaa aag atg gac gac ccc 499
Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu Lys Met Asp Asp Pro
120 125 130
tcg cta ccg ctc gag gat ttt ttg cgt ttc gac gcc gaa ttc cac gtt 547
Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp Ala Glu Phe His Val
135 140 145
gtt atc tcc aaa ggc gcg gaa aac cct ctg atc agt acg ctc atg gaa 595
Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile Ser Thr Leu Met Glu
150 155 160 165

gcc ctc cgt ttg tcc gtg gca gat cac acc gtt gcc agg gcc cgg gcg 643
 Ala Leu Arg Leu Ser Val Ala Asp His Thr Val Ala Arg Ala Arg Ala
 170 175 180

ctc ccc gat tgg cga gcc acc tcg gcg cgt ctg cag aaa gaa cac cgc 691
 Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu Gln Lys Glu His Arg
 185 190 195

gca atc ctc gca gca ctt cgc gca ggc gaa tcc aca gtg gcc gca acc 739
 Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser Thr Val Ala Ala Thr
 200 205 210

ttg atc aaa gaa cac atc gaa ggc tac tac gaa gaa acc gct gcc gcc 787
 Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu Glu Thr Ala Ala Ala
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gag gcc taaatgtccc gcactctgtg ggc 816
 Glu Ala
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 <213> Corynebacterium glutamicum

<400> 168
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Ala Leu Ser Glu Thr Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala
 35 40 45

Leu Arg Val Leu Glu Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser
 50 55 60

Gly Pro Arg Ser Gly Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu
 65 70 75 80

Ser Leu Ser Val Thr Leu Gln Leu Val Thr Asn Gln Val Gly His His
 85 90 95

Asp Ile Tyr Glu Thr Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His
 100 105 110

Ser Ser Ala Glu Arg Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu
 115 120 125

Lys Met Asp Asp Pro Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp
 130 135 140

Ala Glu Phe His Val Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile
 145 150 155 160

Ser Thr Leu Met Glu Ala Leu Arg Leu Ser Val Ala Asp His Thr Val
 165 170 175

Ala	Arg	Ala	Arg 180	Ala	Leu	Pro	Asp 185	Trp	Arg	Ala	Thr	Ser	Ala 190	Arg	Leu
Gln	Lys	Glu 195	His	Arg	Ala	Ile	Leu 200	Ala	Ala	Leu	Arg	Ala 205	Gly	Glu	Ser
Thr	Val 210	Ala	Ala	Thr	Leu	Ile 215	Lys	Glu	His	Ile	Glu 220	Gly	Tyr	Tyr	Glu
Glu 225	Thr	Ala	Ala	Ala	Glu 230	Ala									

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<211> 594
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(571)  
<223> RXA00004
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<400> 169
ttgcaactgtc atgactgtat cccgcgaaga agtgtccctg ccgaqccgaa ctctgaacaa 60

tgccttcggaagatattttc caattcccga tgtagggtca gtg ctg act caa ttg 115
Val Leu Thr Gln Leu
1 5

att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163
Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu
10 15 20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211
Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu
25 30 35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259
Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr
40 45 50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307
Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala
55 60 65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355
Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe
70 75 80 85

gaa ggc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta 403
Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu
90 95 100

gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc 451
Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr
105 110 115

att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta 499
Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu
120 125 130

aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc 547
Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg
135 140 145

cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc 594
Arg Gly Tyr Ile Asn Ser Ala Ala
150 155

<210> 170

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser
1 5 10 15

Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala
20 25 30

Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu
35 40 45

Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln
50 55 60

Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr
65 70 75 80

Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile
85 90 95

Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg
100 105 110

Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser
115 120 125

Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro
130 135 140

Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala
145 150 155

<210> 171

<211> 418

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA01001

<400> 171

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atctccggca ccatccgccg ccgcatcatg aagggggcta gtg acc gtg tcg tgg 115

	Val	Thr	Val	Ser	Trp	
	1				5	
cac caa gca act gac gct cca cca agc atc cgc atc acc acg ctt gcg						163
His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg Ile Thr Thr Leu Ala						
	10				20	
cca tcg ctg cag cct aat cag cgc aaa gtc gcc gaa gtc atg ctt gtc						211
Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala Glu Val Met Leu Val						
	25				35	
gac gcc ccc agc atc gtc gaa ctg acc gct cag ggc ctt gca gat cgc						259
Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln Gly Leu Ala Asp Arg						
	40				50	
gtg ggg gtt ggg cgt gcc acc gtc atc cgc acc gcc cag tcc tta ggc						307
Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr Ala Gln Ser Leu Gly						
	55				65	
tac gac gga ttc ccg cag ctg cgc gtc gcc ctg gcg cag gaa ctg gca						355
Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu Ala Gln Glu Leu Ala						
	70				80	85
ctg gcg cag ggc gcg tcg aga agc atg gtt gaa gga gcg tta agc tcc						403
Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu Gly Ala Leu Ser Ser						
	90				95	100
tcg ttg ctt ggt cat						418
Ser Leu Leu Gly His						
	105					

<210> 172

<211> 106

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Val Thr Val Ser Trp His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg															
1				5				10						15	
Ile Thr Thr Leu Ala Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala															
			20					25					30		
Glu Val Met Leu Val Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln															
			35					40					45		
Gly Leu Ala Asp Arg Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr															
			50					55					60		
Ala Gln Ser Leu Gly Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu															
			65					70					75		80
Ala Gln Glu Leu Ala Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu															
								85					90		95
Gly Ala Leu Ser Ser Ser Leu Leu Gly His															
								100					105		

<210> 173

<211> 1578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1555)
 <223> RXA01375

<400> 173

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cttgaccgac aatctaatta ccgcgaaggg ttagcagcac  gtg act gaa aag tat   115
                                         Val Thr Glu Lys Tyr
                                         1       5

cgt ccc gtc cgt gac att aag cct gct ccg gca gca atg caa tca act   163
Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala Ala Met Gln Ser Thr
                        10                        15                        20

aaa caa gcg ggc cat cct gtg ttc cga agc gtt gtc gct ttt gtt tca   211
Lys Gln Ala Gly His Pro Val Phe Arg Ser Val Val Ala Phe Val Ser
                        25                        30                        35

gtg ctg gtg ttg gtg gta tcg ggt ttg ggg tat ctt gct gtc gga aaa   259
Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr Leu Ala Val Gly Lys
                        40                        45                        50

gtg gat ggt gtc gct tct ggc aac ttg aac ctt ggt ggc ggt cgc ggc   307
Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu Gly Gly Gly Arg Gly
                        55                        60                        65

atc cag gac ggc aat gct gct gac ggt gct acc gat att ttg ttg gtg   355
Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr Asp Ile Leu Leu Val
                        70                        75                        80                        85

ggg tct gat tcc cgt tcc gat gct cag ggc aac acg ctg act gag gag   403
Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn Thr Leu Thr Glu Glu
                        90                        95                        100

gag ctg gcg atg ctc cgc gca ggc gac gag gag aac gac aac acc gat   451
Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu Asn Asp Asn Thr Asp
                        105                        110                        115

acg atc atg gtg att cgt gtt cct aac gat ggt tcc tct gcc acc gct   499
Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly Ser Ser Ala Thr Ala
                        120                        125                        130

gtc gcg att cct cgc gat acc tat att cat gat gac gat tac ggc aac   547
Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp Asp Asp Tyr Gly Asn
                        135                        140                        145

atg aag atc aac ggc gtt tac ggt gcg tac aag gat gcc cgt cgc gct   595
Met Lys Ile Asn Gly Val Tyr Gly Ala Tyr Lys Asp Ala Arg Arg Ala
                        150                        155                        160                        165

gag ctc atg gaa cag ggt ttc acc aat gag tca gag ctg gaa acc cgg   643
Glu Leu Met Glu Gln Gly Phe Thr Asn Glu Ser Glu Leu Glu Thr Arg
                        170                        175                        180

gcg aag gat gct ggc cga gaa ggt ttg atc gat gct gtg tca gat ctc   691

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Ala Lys Asp	Ala Gly Arg	Glu Gly Leu	Ile Asp Ala	Val Ser Asp	Leu	
185		190		195		
acc ggc atc	acc gtc gat	cac tac gcc	gaa gtt ggc	ctt ttg gga	ttc	739
Thr Gly Ile	Thr Val Asp	His Tyr Ala	Glu Val Gly	Leu Leu Gly	Phe	
200		205		210		
gtc ctg ctc	acc gat gct	gtc ggt ggt	gtc gaa gtc	tgc ctc aac	aac	787
Val Leu Leu	Thr Asp Ala	Val Gly Gly	Val Glu Val	Cys Leu Asn	Asn	
215		220		225		
gcc gtc gat	gag cct tta	tcc ggc gcc	aac ttc cct	gca ggc cgt	caa	835
Ala Val Asp	Glu Pro Leu	Ser Gly Ala	Asn Phe Pro	Ala Gly Arg	Gln	
230		235		240	245	
acc ctc ggt	ggc tcc gat	gcg ttg tct	tat gtg cgc	cag cgc cac	gat	883
Thr Leu Gly	Gly Ser Asp	Ala Leu Ser	Tyr Val Arg	Gln Arg His	Asp	
	250		255		260	
ctc ccc cgc	ggc gac ctc	gac cgc atc	gtc cgc cag	cag tcg tat	atg	931
Leu Pro Arg	Gly Asp Leu	Asp Arg Ile	Val Arg Gln	Gln Ser Tyr	Met	
	265		270		275	
gca tcg ctt	gtt aat cag	gtg ctg tct	tct gga aca	ctc acc aac	cct	979
Ala Ser Leu	Val Asn Gln	Val Leu Ser	Ser Gly Thr	Leu Thr Asn	Pro	
	280		285		290	
gca aag ctt	tcc gca ctt	gct gat gcc	gtc acc cgc	tcc gtc gtc	atc	1027
Ala Lys Leu	Ser Ala Leu	Ala Asp Ala	Val Thr Arg	Ser Val Val	Ile	
	295		300		305	
gac gaa ggc	tgg gag atc	atg agc ttt	gcc act cag	ctg cag aac	ctc	1075
Asp Glu Gly	Trp Glu Ile	Met Ser Phe	Ala Thr Gln	Leu Gln Asn	Leu	
310		315		320	325	
gcg ggc ggc	aac gtc aca	ttt gcc acc	atc ccg gtt	acc tct atc	gac	1123
Ala Gly Gly	Asn Val Thr	Phe Ala Thr	Ile Pro Val	Thr Ser Ile	Asp	
	330		335		340	
ggc acc ggc	gat tac ggc	gag tcc gtt	gtc acc atc	gat gtc aac	cag	1171
Gly Thr Gly	Asp Tyr Gly	Glu Ser Val	Val Thr Ile	Asp Val Asn	Gln	
	345		350		355	
gtg cat gca	ttc ttc caa	gaa gca ctc	ggc gaa gca	gag cca gct	cca	1219
Val His Ala	Phe Phe Gln	Glu Ala Leu	Gly Glu Ala	Glu Pro Ala	Pro	
	360		365		370	
gaa gac ggc	tcc gac gat	caa tct gct	gat cag gcc	cct gac cta	agc	1267
Glu Asp Gly	Ser Asp Asp	Gln Ser Ala	Asp Gln Ala	Pro Asp Leu	Ser	
	375		380		385	
gaa gtc gag	gtc cac gtc	ctc aac gct	tcc tac gtc	gaa ggc ctc	gcc	1315
Glu Val Glu	Val His Val	Leu Asn Ala	Ser Tyr Val	Glu Gly Leu	Ala	
390		395		400	405	
aac ggt atc	gcc gcg caa	ctg cag gaa	ttg ggt tac	tcc atc gca	gag	1363
Asn Gly Ile	Ala Ala Gln	Leu Gln Glu	Leu Gly Tyr	Ser Ile Ala	Glu	
	410		415		420	
acc ggc aac	gca gcg gaa	ggc ctc tac	tac gag tcc	cag atc ctc	gcc	1411
Thr Gly Asn	Ala Ala Glu	Gly Leu Tyr	Tyr Tyr Glu	Ser Gln Ile	Leu Ala	

425	430	435	
gcc gaa gaa gac agc gcc aag gcc ctc gcg att tcc gaa gcc ctc ggt			1459
Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile Ser Glu Ala Leu Gly			
440	445	450	
ggt ctc cca tcg tgg cca act ctt ccc tcg acg aca aca ccg tca tcg			1507
Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr Thr Thr Pro Ser Ser			
455	460	465	
tcg tat ccg ccg gcg att acg ctg gcc cta ccg cgg aag caa acg ccg			1555
Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro Arg Lys Gln Thr Pro			
470	475	480	485
tgacatccag caccgtcggc cag			1578

<210> 174

<211> 485

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

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20 25 30	
Val Ala Phe Val Ser Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr	
35 40 45	
Leu Ala Val Gly Lys Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu	
50 55 60	
Gly Gly Gly Arg Gly Ile Gln Asp Gly Asn Ala Ala Asp Gly Ala Thr	
65 70 75 80	
Asp Ile Leu Leu Val Gly Ser Asp Ser Arg Ser Asp Ala Gln Gly Asn	
85 90 95	
Thr Leu Thr Glu Glu Glu Leu Ala Met Leu Arg Ala Gly Asp Glu Glu	
100 105 110	
Asn Asp Asn Thr Asp Thr Ile Met Val Ile Arg Val Pro Asn Asp Gly	
115 120 125	
Ser Ser Ala Thr Ala Val Ala Ile Pro Arg Asp Thr Tyr Ile His Asp	
130 135 140	
Asp Asp Tyr Gly Asn Met Lys Ile Asn Gly Val Tyr Gly Ala Tyr Lys	
145 150 155 160	
Asp Ala Arg Arg Ala Glu Leu Met Glu Gln Gly Phe Thr Asn Glu Ser	
165 170 175	
Glu Leu Glu Thr Arg Ala Lys Asp Ala Gly Arg Glu Gly Leu Ile Asp	
180 185 190	
Ala Val Ser Asp Leu Thr Gly Ile Thr Val Asp His Tyr Ala Glu Val	
195 200 205	

Gly Leu Leu Gly Phe Val Leu Leu Thr Asp Ala Val Gly Gly Val Glu
 210 215 220
 Val Cys Leu Asn Asn Ala Val Asp Glu Pro Leu Ser Gly Ala Asn Phe
 225 230 235 240
 Pro Ala Gly Arg Gln Thr Leu Gly Gly Ser Asp Ala Leu Ser Tyr Val
 245 250 255
 Arg Gln Arg His Asp Leu Pro Arg Gly Asp Leu Asp Arg Ile Val Arg
 260 265 270
 Gln Gln Ser Tyr Met Ala Ser Leu Val Asn Gln Val Leu Ser Ser Gly
 275 280 285
 Thr Leu Thr Asn Pro Ala Lys Leu Ser Ala Leu Ala Asp Ala Val Thr
 290 295 300
 Arg Ser Val Val Ile Asp Glu Gly Trp Glu Ile Met Ser Phe Ala Thr
 305 310 315 320
 Gln Leu Gln Asn Leu Ala Gly Gly Asn Val Thr Phe Ala Thr Ile Pro
 325 330 335
 Val Thr Ser Ile Asp Gly Thr Gly Asp Tyr Gly Glu Ser Val Val Thr
 340 345 350
 Ile Asp Val Asn Gln Val His Ala Phe Phe Gln Glu Ala Leu Gly Glu
 355 360 365
 Ala Glu Pro Ala Pro Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln
 370 375 380
 Ala Pro Asp Leu Ser Glu Val Glu Val His Val Leu Asn Ala Ser Tyr
 385 390 395 400
 Val Glu Gly Leu Ala Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly
 405 410 415
 Tyr Ser Ile Ala Glu Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu
 420 425 430
 Ser Gln Ile Leu Ala Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile
 435 440 445
 Ser Glu Ala Leu Gly Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr
 450 455 460
 Thr Thr Pro Ser Ser Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro
 465 470 475 480
 Arg Lys Gln Thr Pro
 485

<210> 175

<211> 508

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02831

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gcttcgatag ggctaggaaa accctgtcgg aggagcgccc atg aca cat cgg atc 115
 Met Thr His Arg Ile
 1 5

aca ccc gaa ctc tcg gcc gaa ttg cgg ggg gtg gcc cac agc ctt gca 163
 Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val Ala His Ser Leu Ala
 10 15 20

gat gcg gcg cgg ccc gtc acc ttg caa tac ttc cgc aca gca gtc gcg 211
 Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe Arg Thr Ala Val Ala
 25 30 35

gca gat aac aaa ggc gcg ctg cgc ggg atg gct tac gac ccc gtc acc 259
 Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala Tyr Asp Pro Val Thr
 40 45 50

att gcc gac cgt gca agc gaa cag gcc atg cgt gac att ctg gcc cgt 307
 Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg Asp Ile Leu Ala Arg
 55 60 65

cta cgc ccc gat gat gcg atc ttg ggt gaa gaa ttc ggc ccc aaa gcg 355
 Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu Phe Gly Pro Lys Ala
 70 75 80 85

ggc aca acg ggc ctc aca tgg gtg ctg gac ccg att gac ggc act cgc 403
 Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro Ile Asp Gly Thr Arg
 90 95 100

gca tat atc gcg ggc gcg ccc act tgg ggc gtg ctg atc gca gta tcg 451
 Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val Leu Ile Ala Val Ser
 105 110 115

gat gat cag ggc ccg ctg ttc ggt atc gtc gac caa ccc tat att ggc 499
 Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp Gln Pro Tyr Ile Gly
 120 125 130

gag cgt ttt 508
 Glu Arg Phe
 135

<210> 176

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Thr His Arg Ile Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val
 1 5 10 15

Ala His Ser Leu Ala Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe
 20 25 30

<400> 177																
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caaagcaatc tagctgacga cccaatatag tcctgtcatt																
Met Leu Ala Ile Val																115
1 5																
cag cta tca aaa gaa tct att att ggc gca gcc gtt tcg atc ttg agc																163
Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala Val Ser Ile Leu Ser																
10 15 20																
gaa ttc ggt ttg tcg gat atg acc atg cgc cgc gtc gca aag cag tta																211
Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg Val Ala Lys Gln Leu																
25 30 35																
aat gtc gcg ccg ggc gcg ctg tat tgg cat ttt aaa aat aag cag gag																259
Asn Val Ala Pro Gly Ala Leu Tyr Trp His Phe Lys Asn Lys Gln Glu																
40 45 50																
ctt atc gac gcc acc tcg cgc tat ctc ctc gcg cct gtc ttg ggg cgc																307
Leu Ile Asp Ala Thr Ser Arg Tyr Leu Leu Ala Pro Val Leu Gly Arg																
55 60 65																
aac gac gag cag cga gca agc att tcc gcg cag gaa acc tgc gcg gaa																355
Asn Asp Glu Gln Arg Ala Ser Ile Ser Ala Gln Glu Thr Cys Ala Glu																
70 75 80 85																
atg cgt tcg ctg atg atg caa acc aaa gat ggt gcg gaa gtc atc agt																403
Met Arg Ser Leu Met Met Gln Thr Lys Asp Gly Ala Glu Val Ile Ser																

90										95					100					
gcc	gca	ctg	agt	aat	cag	caa	ttg	cgc	caa	gaa	ttg	gaa	tca	ctc	att	451				
Ala	Ala	Leu	Ser	Asn	Gln	Gln	Leu	Arg	Gln	Glu	Leu	Glu	Ser	Leu	Ile					
			105					110					115							
tct	gac	tct	tta	aag	gaa	cct	aat	gag	gtt	ggc	gct	ttt	acg	ctg	cta	499				
Ser	Asp	Ser	Leu	Lys	Glu	Pro	Asn	Glu	Val	Gly	Ala	Phe	Thr	Leu	Leu					
		120					125					130								
cat	ttt	gtg	gtg	ggg	gca	gta	tta	aca	gaa	caa	act	cag	ctg	cag	atg	547				
His	Phe	Val	Val	Gly	Ala	Val	Leu	Thr	Glu	Gln	Thr	Gln	Leu	Gln	Met					
	135					140					145									
cac	gag	ttc	acg	gct	ggc	gcg	gga	gat	gac	acg	caa	gaa	aac	cct	gcc	595				
His	Glu	Phe	Thr	Ala	Gly	Ala	Gly	Asp	Asp	Thr	Gln	Glu	Asn	Pro	Ala					
150					155					160					165					
gat	gca	aac	ttt	gag	gag	aga	ttc	aat	caa	gga	ata	gaa	atc	att	ctg	643				
Asp	Ala	Asn	Phe	Glu	Glu	Arg	Phe	Asn	Gln	Gly	Ile	Glu	Ile	Ile	Leu					
				170				175						180						
gtg	ggg	cta	gac	gcg	ctt	ggg	cat	ata	aga	tgacgttcca	tgacatcaac	gat				696				
Val	Gly	Leu	Asp	Ala	Leu	Gly	His	Ile	Arg											
			185				190													

<210> 178

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Met	Leu	Ala	Ile	Val	Gln	Leu	Ser	Lys	Glu	Ser	Ile	Ile	Gly	Ala	Ala	
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Val	Ser	Ile	Leu	Ser	Glu	Phe	Gly	Leu	Ser	Asp	Met	Thr	Met	Arg	Arg	
			20					25					30			
Val	Ala	Lys	Gln	Leu	Asn	Val	Ala	Pro	Gly	Ala	Leu	Tyr	Trp	His	Phe	
		35				40						45				
Lys	Asn	Lys	Gln	Glu	Leu	Ile	Asp	Ala	Thr	Ser	Arg	Tyr	Leu	Leu	Ala	
	50					55					60					
Pro	Val	Leu	Gly	Arg	Asn	Asp	Glu	Gln	Arg	Ala	Ser	Ile	Ser	Ala	Gln	
	65				70				75						80	
Glu	Thr	Cys	Ala	Glu	Met	Arg	Ser	Leu	Met	Met	Gln	Thr	Lys	Asp	Gly	
				85					90					95		
Ala	Glu	Val	Ile	Ser	Ala	Ala	Leu	Ser	Asn	Gln	Gln	Leu	Arg	Gln	Glu	
			100					105					110			
Leu	Glu	Ser	Leu	Ile	Ser	Asp	Ser	Leu	Lys	Glu	Pro	Asn	Glu	Val	Gly	
		115					120					125				
Ala	Phe	Thr	Leu	Leu	His	Phe	Val	Val	Gly	Ala	Val	Leu	Thr	Glu	Gln	
	130					135					140					

Thr Gln Leu Gln Met His Glu Phe Thr Ala Gly Ala Gly Asp Asp Thr
145 150 155 160

Gln Glu Asn Pro Ala Asp Ala Asn Phe Glu Glu Arg Phe Asn Gln Gly
165 170 175

Ile Glu Ile Ile Leu Val Gly Leu Asp Ala Leu Gly His Ile Arg
180 185 190

<210> 179

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXA00253

<400> 179

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cgctggttgt cttgtagaaa aaggcgtaac gtcataataac atg cct agc gaa act 115
Met Pro Ser Glu Thr
1 5

atg aaa cca gcc gta gcg tca act ctg gcg gcc act tcc acg gga cgt 163
Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala Thr Ser Thr Gly Arg
10 15 20

cgt cct gga cgc ccc acc caa cgt atc ctt tcc gtc gaa tcc ata gtg 211
Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser Val Glu Ser Ile Val
25 30 35

gag cgc act tta aac att gcc ggc cgc gaa gga ttc gct gcc gtg acc 259
Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly Phe Ala Ala Val Thr
40 45 50

atg aac cgc ctc gcc cga gac atg ggt gtc acc cct cgc gca ctg tat 307
Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr Pro Arg Ala Leu Tyr
55 60 65

aac cat gtg cta aat cgt caa gaa atc att gat cgc gtc tgg gtg cgc 355
Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp Arg Val Trp Val Arg
70 75 80 85

atc atc gat gat atc aag gtg ccc gat ctt gat ccg gac aat tgg cgg 403
Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp Pro Asp Asn Trp Arg
90 95 100

caa tct att cat acg ctg tgg agc tca ttg cgc gac caa ttc cgt gag 451
Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg Asp Gln Phe Arg Glu
105 110 115

act cca cgt gtt ctt ctg gtc gcg ctg gat gaa cag atc tct act cag 499
Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu Gln Ile Ser Thr Gln
120 125 130

ggc act tcc cca ctg cga atc gcg ggt gcg gag gag tcc ttg aag ttc 547
Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu Glu Ser Leu Lys Phe

135	140	145	
ttg act gat atc ggg ctg tcc ctc aag gaa gca acc atc atc cgg gag			595
Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala Thr Ile Ile Arg Glu			
150	155	160	165
atg atg atg gct gat gtc ttc agc ttc acc ctg act tct gac tac acc			643
Met Met Met Ala Asp Val Phe Ser Phe Thr Leu Thr Ser Asp Tyr Thr			
	170	175	180
ttt gac aat cgt cca gag ggc gaa aag ccg gat gtg ttt gct ccg gtt			691
Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp Val Phe Ala Pro Val			
	185	190	195
cct aag cca tgg ctt gat gag aac cca gat gtg gaa gcg cca ctg acc			739
Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val Glu Ala Pro Leu Thr			
	200	205	210
cgt aaa gca gtc gaa gag tcc gtc tca act tct gac gaa ctc ttc ggc			787
Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser Asp Glu Leu Phe Gly			
	215	220	225
tac atg gtg gag gct cgc att gct tat att gaa aag ctg ctt gcc gcc			835
Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu Lys Leu Leu Ala Ala			
	230	235	240
aaa tagtttctaa aggttattga ggg			861
Lys			

<210> 180

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Pro Ser Glu Thr Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala			
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Thr Ser Thr Gly Arg Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser			
	20	25	30
Val Glu Ser Ile Val Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly			
	35	40	45
Phe Ala Ala Val Thr Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr			
	50	55	60
Pro Arg Ala Leu Tyr Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp			
	65	70	75
Arg Val Trp Val Arg Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp			
	85	90	95
Pro Asp Asn Trp Arg Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg			
	100	105	110
Asp Gln Phe Arg Glu Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu			
	115	120	125

Gln Ile Ser Thr Gln Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu
 130 135 140

Glu Ser Leu Lys Phe Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala
 145 150 155 160

Thr Ile Ile Arg Glu Met Met Met Ala Asp Val Phe Ser Phe Thr Leu
 165 170 175

Thr Ser Asp Tyr Thr Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp
 180 185 190

Val Phe Ala Pro Val Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val
 195 200 205

Glu Ala Pro Leu Thr Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser
 210 215 220

Asp Glu Leu Phe Gly Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu
 225 230 235 240

Lys Leu Leu Ala Ala Lys
 245

<210> 181
 <211> 888
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(865)
 <223> RXA01118

<400> 181
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acaagggttc gcaatgcgaa caaaaagagg agttgatggg atg gtc gaa caa tcg 115
 Met Val Glu Gln Ser
 1 5

cca gat ttc gta caa tca ttt gcc cgc ggc tta tct gtg atc cga agt 163
 Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu Ser Val Ile Arg Ser
 10 15 20

ttc agc gca gat aat cca tcg caa aca ctg tcc gaa gtc gcc agc caa 211
 Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser Glu Val Ala Ser Gln
 25 30 35

act gga ctc tca agg gcc acc gct agg cgc ttt ctc cac acc ttg acc 259
 Thr Gly Leu Ser Arg Ala Thr Ala Arg Arg Phe Leu His Thr Leu Thr
 40 45 50

gac ctt gga tat gcg gta aac aac gat tcc cgg ttc cag ctc aca cca 307
 Asp Leu Gly Tyr Ala Val Asn Asn Asp Ser Arg Phe Gln Leu Thr Pro
 55 60 65

cgt gtt ttg gag ctt gga gca agc tac ctt tcc gca ttg tcc ctg cct 355
 Arg Val Leu Glu Leu Gly Ala Ser Tyr Leu Ser Ala Leu Ser Leu Pro
 70 75 80 85

gcg atc gcg cag ccc cgc ctg gag gta ctc tcc cgc cag gtc ggc gaa 403
 Ala Ile Ala Gln Pro Arg Leu Glu Val Leu Ser Arg Gln Val Gly Glu
 90 95 100

tca agc tcc atg tcc gta ctc gac ggc act gac atc atc tac gtt tgc 451
 Ser Ser Ser Met Ser Val Leu Asp Gly Thr Asp Ile Ile Tyr Val Cys
 105 110 115

cgc gtt ccg gtg cgc cgc atc atg acg gtg aac atc acc atc ggc acc 499
 Arg Val Pro Val Arg Arg Ile Met Thr Val Asn Ile Thr Ile Gly Thr
 120 125 130

cgt ttc cct gcg tac gcc acc tcc atg gga cgc atc atg ctg gcc aac 547
 Arg Phe Pro Ala Tyr Ala Thr Ser Met Gly Arg Ile Met Leu Ala Asn
 135 140 145

ctt ccc gaa gaa gaa tta gat gaa atg ctg gcg gcg gca ccc cct gaa 595
 Leu Pro Glu Glu Glu Leu Asp Glu Met Leu Ala Ala Ala Pro Pro Glu
 150 155 160 165

cag ttg acc acc cgg tca ctg acc tcc atc gcc tca atc cgg gaa gag 643
 Gln Leu Thr Thr Arg Ser Leu Thr Ser Ile Ala Ser Ile Arg Glu Glu
 170 175 180

atc att gct acc cgc gaa agg ggg tgg tca ttg gtg gat cag gag ctc 691
 Ile Ile Ala Thr Arg Glu Arg Gly Trp Ser Leu Val Asp Gln Glu Leu
 185 190 195

gag ccg ggc ctg cgt tcg ctc gcg gcg ccg atc acc aat gcc cag ggc 739
 Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile Thr Asn Ala Gln Gly
 200 205 210

gaa gtg gtt gct tcc atc aat gtg tcg acc caa tcg gca tca cat tcg 787
 Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln Ser Ala Ser His Ser
 215 220 225

gtg gaa gat atc cgc aag ctg gtg ctg ccg cag ctt tta gaa acg gct 835
 Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln Leu Leu Glu Thr Ala
 230 235 240 245

caa gca att tcg aca gat ctc tct gca ctc taaattaagg atcaaaaaat gaa 888
 Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
 250 255

<210> 182

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Met Val Glu Gln Ser Pro Asp Phe Val Gln Ser Phe Ala Arg Gly Leu
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Ser Val Ile Arg Ser Phe Ser Ala Asp Asn Pro Ser Gln Thr Leu Ser
 20 25 30

Glu Val Ala Ser Gln Thr Gly Leu Ser Arg Ala Thr Ala Arg Arg Phe
 35 40 45

Leu His Thr Leu Thr Asp Leu Gly Tyr Ala Val Asn Asn Asp Ser Arg
 50 55 60
 Phe Gln Leu Thr Pro Arg Val Leu Glu Leu Gly Ala Ser Tyr Leu Ser
 65 70 75 80
 Ala Leu Ser Leu Pro Ala Ile Ala Gln Pro Arg Leu Glu Val Leu Ser
 85 90 95
 Arg Gln Val Gly Glu Ser Ser Ser Met Ser Val Leu Asp Gly Thr Asp
 100 105 110
 Ile Ile Tyr Val Cys Arg Val Pro Val Arg Arg Ile Met Thr Val Asn
 115 120 125
 Ile Thr Ile Gly Thr Arg Phe Pro Ala Tyr Ala Thr Ser Met Gly Arg
 130 135 140
 Ile Met Leu Ala Asn Leu Pro Glu Glu Glu Leu Asp Glu Met Leu Ala
 145 150 155 160
 Ala Ala Pro Pro Glu Gln Leu Thr Thr Arg Ser Leu Thr Ser Ile Ala
 165 170 175
 Ser Ile Arg Glu Glu Ile Ile Ala Thr Arg Glu Arg Gly Trp Ser Leu
 180 185 190
 Val Asp Gln Glu Leu Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile
 195 200 205
 Thr Asn Ala Gln Gly Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln
 210 215 220
 Ser Ala Ser His Ser Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln
 225 230 235 240
 Leu Leu Glu Thr Ala Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
 245 250 255

<210> 183

<211> 654

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(654)

<223> RXA01840

<400> 183

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 Ile Ser Glu Glu Asp Gly Ala Ser Glu Pro Ala Thr Phe Ala Glu Arg
 1 5 10 15
 tcc caa cgc ctc atc cag cag gaa tgc gtt gca gcc gtg ttt ggt gga 96
 Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly
 20 25 30
 tgg acc tcc gcc tcc cgc aaa gca atg ctc ccc gtc ttt gag ggc aat 144

Trp	Thr	Ser	Ala	Ser	Arg	Lys	Ala	Met	Leu	Pro	Val	Phe	Glu	Gly	Asn		
		35					40					45					
aac	tcc	ctg	ctg	ttc	tac	ccg	gtg	cag	tac	gag	ggc	atg	gaa	tcc	tcg	192	
Asn	Ser	Leu	Leu	Phe	Tyr	Pro	Val	Gln	Tyr	Glu	Gly	Met	Glu	Ser	Ser		
	50					55				60							
ccg	aat	att	ttc	tac	acc	ggc	gcc	acc	acc	aac	cag	cag	atc	atc	ccg	240	
Pro	Asn	Ile	Phe	Tyr	Thr	Gly	Ala	Thr	Thr	Asn	Gln	Gln	Ile	Ile	Pro		
	65				70					75					80		
gct	ctt	gat	tac	ctg	cgt	gaa	aac	ggc	ctg	aac	cgc	ctt	ttc	ctt	gtc	288	
Ala	Leu	Asp	Tyr	Leu	Arg	Glu	Asn	Gly	Leu	Asn	Arg	Leu	Phe	Leu	Val		
				85					90					95			
ggc	tcc	gat	tat	gtt	ttc	cca	cgc	act	gca	aat	tcc	atc	atc	aag	gac	336	
Gly	Ser	Asp	Tyr	Val	Phe	Pro	Arg	Thr	Ala	Asn	Ser	Ile	Ile	Lys	Asp		
			100					105					110				
tac	gcc	gaa	gcc	aat	ggc	atg	gaa	atc	gtc	ggc	gaa	gac	tac	gcg	ccg	384	
Tyr	Ala	Glu	Ala	Asn	Gly	Met	Glu	Ile	Val	Gly	Glu	Asp	Tyr	Ala	Pro		
		115					120					125					
ttg	gga	tcc	acc	gac	ttc	acc	acc	atc	gcc	aac	cgc	atg	cgt	gac	tcc	432	
Leu	Gly	Ser	Thr	Asp	Phe	Thr	Thr	Ile	Ala	Asn	Arg	Met	Arg	Asp	Ser		
	130					135					140						
aac	gca	gat	gcc	gtg	ttc	aac	act	ttg	aat	ggc	gat	tcc	aac	gtg	gcg	480	
Asn	Ala	Asp	Ala	Val	Phe	Asn	Thr	Leu	Asn	Gly	Asp	Ser	Asn	Val	Ala		
	145				150					155					160		
ttc	ttc	cgc	cag	tac	aac	agc	ctc	ggc	ttc	aat	gca	gac	acc	ctt	ccg	528	
Phe	Phe	Arg	Gln	Tyr	Asn	Ser	Leu	Gly	Phe	Asn	Ala	Asp	Thr	Leu	Pro		
				165				170						175			
gtg	atg	tca	gta	tcc	att	gcg	gaa	gaa	gaa	gtc	gga	ggc	atc	ggc	acc	576	
Val	Met	Ser	Val	Ser	Ile	Ala	Glu	Glu	Glu	Val	Gly	Gly	Ile	Gly	Thr		
			180					185					190				
gca	aat	att	gag	ggc	cag	ctg	gtg	gcg	tgg	gac	tac	tac	caa	acc	atc	624	
Ala	Asn	Ile	Glu	Gly	Gln	Leu	Val	Ala	Trp	Asp	Tyr	Tyr	Gln	Thr	Ile		
		195					200					205					
gac	acc	cca	gaa	aac	gag	acc	ttc	gtg	gag							654	
Asp	Thr	Pro	Glu	Asn	Glu	Thr	Phe	Val	Glu								
	210					215											

<210> 184

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Ile	Ser	Glu	Glu	Asp	Gly	Ala	Ser	Glu	Pro	Ala	Thr	Phe	Ala	Glu	Arg
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Ser	Gln	Arg	Leu	Ile	Gln	Gln	Glu	Cys	Val	Ala	Ala	Val	Phe	Gly	Gly
			20					25					30		

Trp	Thr	Ser	Ala	Ser	Arg	Lys	Ala	Met	Leu	Pro	Val	Phe	Glu	Gly	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45					
Asn	Ser	Leu	Leu	Phe	Tyr	Pro	Val	Gln	Tyr	Glu	Gly	Met	Glu	Ser	Ser
50						55					60				
Pro	Asn	Ile	Phe	Tyr	Thr	Gly	Ala	Thr	Thr	Asn	Gln	Gln	Ile	Ile	Pro
65					70					75					80
Ala	Leu	Asp	Tyr	Leu	Arg	Glu	Asn	Gly	Leu	Asn	Arg	Leu	Phe	Leu	Val
				85					90					95	
Gly	Ser	Asp	Tyr	Val	Phe	Pro	Arg	Thr	Ala	Asn	Ser	Ile	Ile	Lys	Asp
			100					105					110		
Tyr	Ala	Glu	Ala	Asn	Gly	Met	Glu	Ile	Val	Gly	Glu	Asp	Tyr	Ala	Pro
		115					120					125			
Leu	Gly	Ser	Thr	Asp	Phe	Thr	Thr	Ile	Ala	Asn	Arg	Met	Arg	Asp	Ser
	130					135					140				
Asn	Ala	Asp	Ala	Val	Phe	Asn	Thr	Leu	Asn	Gly	Asp	Ser	Asn	Val	Ala
145					150					155					160
Phe	Phe	Arg	Gln	Tyr	Asn	Ser	Leu	Gly	Phe	Asn	Ala	Asp	Thr	Leu	Pro
			165						170					175	
Val	Met	Ser	Val	Ser	Ile	Ala	Glu	Glu	Glu	Val	Gly	Gly	Ile	Gly	Thr
			180					185					190		
Ala	Asn	Ile	Glu	Gly	Gln	Leu	Val	Ala	Trp	Asp	Tyr	Tyr	Gln	Thr	Ile
		195				200					205				
Asp	Thr	Pro	Glu	Asn	Glu	Thr	Phe	Val	Glu						
	210					215									

<210> 185

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXA00400

<400> 185

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tgagggcttc	cccacccgca	attaattaat	tggagttttg	ttg	ttc	act	ctt	gaa	115
				Leu	Phe	Thr	Leu	Glu	
				1				5	

cag	ttg	cgg	tgt	ttt	gtc	gcc	gtc	gcc	aat	cat	ctt	cat	ttc	gga	aaa	163
Gln	Leu	Arg	Cys	Phe	Val	Ala	Val	Ala	Asn	His	Leu	His	Phe	Gly	Lys	
				10				15						20		

gct	gct	gca	gag	cta	tcc	atg	acg	cag	ccg	ccg	ttg	agt	cgt	cag	att	211
Ala	Ala	Ala	Glu	Leu	Ser	Met	Thr	Gln	Pro	Pro	Leu	Ser	Arg	Gln	Ile	
			25					30					35			

caa aag ctg gag aag atc gtc ggt gca acc ctg ctt gat cgt gac aac	259
Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu Leu Asp Arg Asp Asn	
40 45 50	
cgc aag gtg gaa ctg acc act gcg ggt ttc gca ttt ttg aag gat gct	307
Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala Phe Leu Lys Asp Ala	
55 60 65	
cgc ctc att ctc aat tcc acc gag aag gcg gct gag cgc gca cga ttg	355
Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala Glu Arg Ala Arg Leu	
70 75 80 85	
gct agc tct ggc atg tgg gga cag ctc aat att gga tac acc gct gca	403
Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile Gly Tyr Thr Ala Ala	
90 95 100	
gcg ggt ttt tcc att ctg ggc ccg acg ttg aat cag ttg cat gag aag	451
Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn Gln Leu His Glu Lys	
105 110 115	
atg ccg ggg gtc agt gtc gat ctt ttt gag atg gtc tcc acc gag cag	499
Met Pro Gly Val Ser Val Asp Leu Phe Glu Met Val Ser Thr Glu Gln	
120 125 130	
atc gcc gcc ttg gaa tct ggg cta ctg gat ctt ggc att ggc cga ttg	547
Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu Gly Ile Gly Arg Leu	
135 140 145	
agc tcg cca gtt gag ggt ctt caa act cga cgt ctc cag gca gat tcc	595
Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg Leu Gln Ala Asp Ser	
150 155 160 165	
ttg gtt ctt gca gct ccg aag ggg cat cca ctt ctt gat cag aat cga	643
Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu Leu Asp Gln Asn Arg	
170 175 180	
cca ctg ttg cgg aag cat ctg act ggg gtt cct ttt ctg cag cac tct	691
Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro Phe Leu Gln His Ser	
185 190 195	
ccc acc aag gcg aag tac ctc tac gac atc gtt gtt aga aac ttc acg	739
Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val Val Arg Asn Phe Thr	
200 205 210	
atc aat gat gcg cag gtg caa cat acg ctg agc cag atc acc acg atg	787
Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser Gln Ile Thr Thr Met	
215 220 225	
gtt agt ctg gtg gcc tct gga ctg ggt gtt gcg ctg gtt ccg gag tct	835
Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala Leu Val Pro Glu Ser	
230 235 240 245	
gcg aaa aaa ctc aat tac agc ggt gtt gag tat cgc cat ttt tat gat	883
Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr Arg His Phe Tyr Asp	
250 255 260	
cta cct gtt ggt tta gcg gag ctg cag gct att tat tcc acc tcg aat	931
Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile Tyr Ser Thr Ser Asn	
265 270 275	
gat aat cct gcg gtg cgg aaa ttc atc aaa aac att gac gat acc ttt	979

Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn Ile Asp Asp Thr Phe
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taagcatttc aacatgccaa act

1002

<210> 186

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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Leu His Phe Gly Lys Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro
 20 25 30

Leu Ser Arg Gln Ile Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu
 35 40 45

Leu Asp Arg Asp Asn Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala
 50 55 60

Phe Leu Lys Asp Ala Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala
 65 70 75 80

Glu Arg Ala Arg Leu Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile
 85 90 95

Gly Tyr Thr Ala Ala Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn
 100 105 110

Gln Leu His Glu Lys Met Pro Gly Val Ser Val Asp Leu Phe Glu Met
 115 120 125

Val Ser Thr Glu Gln Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu
 130 135 140

Gly Ile Gly Arg Leu Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg
 145 150 155 160

Leu Gln Ala Asp Ser Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu
 165 170 175

Leu Asp Gln Asn Arg Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro
 180 185 190

Phe Leu Gln His Ser Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val
 195 200 205

Val Arg Asn Phe Thr Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser
 210 215 220

Gln Ile Thr Thr Met Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala
 225 230 235 240

Leu Val Pro Glu Ser Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr
 245 250 255

Arg His Phe Tyr Asp Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile

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<211> 1500
<212> DNA
<213> Corynebacterium glutamicum
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<220>
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<222> (101) .. (1477)
<223> BXA02787
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<400> 187																
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gttgcttggt tgtttcagcc aagcgactaa cctgtgcact																115
Met Ala Gln Asp Ser																5
1																
ctt ttt gaa acg ccc gaa aca ccg gga tcc gca ggc aac aca agc agc																163
Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala Gly Asn Thr Ser Ser																20
10 15																
gtg agc aat tcc aaa gcc gcc tcg aag tat ttt cac cca ggc gga cac																211
Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe His Pro Gly Gly His																35
25 30																
gca ccc ctt gct gcc cgc atg agg cca agg acg ctt gat gaa gtg gtt																259
Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr Leu Asp Glu Val Val																50
40 45																
ggc caa cag cat ttg ctg ggg gag gcc agg cca ctt cgc cgg ctc att																307
Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro Leu Arg Arg Leu Ile																65
55 60																
gaa ggt tca ggg gat gcc tcc gtc att ttg tat ggg cct ccc ggc act																355
Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr Gly Pro Pro Gly Thr																85
70 75 80																
gga aaa aca acc att gcc tca ttg att tct gca gct gca ggc gat cgc																403
Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala Ala Ala Gly Asp Arg																100
90 95																
ttt gtg gcg atg tcg gcg ctg tcc tca ggt gtg aaa gaa gtc cgc gcc																451
Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val Lys Glu Val Arg Ala																115
105 110																
gtt att gaa cgt gcg agg atg gat ctg caa tta ggg cag cgc acc gtg																499
Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu Gly Gln Arg Thr Val																130
120 125 130																
ctg ttt att gat gag gtt cat agg ttt tcc aaa act cag cag gac gcg																547
Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys Thr Gln Gln Asp Ala																145
135 140 145																

ttg ctc tct gca gtg gaa aac cgc acc gtg ttg ctc gtt gca gcg acc	595
Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu Leu Val Ala Ala Thr	
150 155 160 165	
act gag aac ccc tcc ttt tca gtg gtg tct cca ctg ctg tcc agg tcc	643
Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro Leu Leu Ser Arg Ser	
170 175 180	
ttg ctg ctc cag ttg gaa tct tta agc gat gag gat att aaa aca gtc	691
Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu Asp Ile Lys Thr Val	
185 190 195	
ctt aat aaa gcg ctt gaa gat gag cgt gga ctt gcc ggt cga atc acc	739
Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu Ala Gly Arg Ile Thr	
200 205 210	
gcc acc gat gaa gca gtt gac cag ttg gtt ctt ctt gcc ggt ggc gat	787
Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu Leu Ala Gly Gly Asp	
215 220 225	
gcc cgc cga ggc ctg acc tac att gaa gcc gct gca gaa gcc gta gaa	835
Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala Glu Ala Val Glu	
230 235 240 245	
gat ggc ggc gtt tta gat att gac acc gtc atg gcc aac gtg aac cgc	883
Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met Ala Asn Val Asn Arg	
250 255 260	
gca gtg gtc cgc tat gac cgc gat ggc gat cag cac tat gac gtg gtc	931
Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln His Tyr Asp Val Val	
265 270 275	
agt gcc tgg atc aaa tca att aga ggc tcc gat gta gac gca gcc ttg	979
Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp Val Asp Ala Ala Leu	
280 285 290	
cac tac ttg gcg cgc atg att gat gcc ggt gaa gac cca cgg ttt att	1027
His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu Asp Pro Arg Phe Ile	
295 300 305	
gcc cgc cgg ttg gtg gtt cac tca agt gaa gac atc ggt atg gct gat	1075
Ala Arg Arg Leu Val Val His Ser Ser Glu Asp Ile Gly Met Ala Asp	
310 315 320 325	
cct tcg gcc atg caa gtg gcc att gct gca gct caa gct gtc caa tta	1123
Pro Ser Ala Met Gln Val Ala Ile Ala Ala Gln Ala Val Gln Leu	
330 335 340	
atc ggt atg cca gag gcg cgg atc aat ttg gcg caa gcg acc att cat	1171
Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala Gln Ala Thr Ile His	
345 350 355	
ttg gct ctt gct ccc aaa tcc aat gct gtc atc atg gcc atg gat gct	1219
Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile Met Ala Met Asp Ala	
360 365 370	
gct ttg act gat gtt cag caa ggc cac atc ggt acc gtt cct gcg cat	1267
Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly Thr Val Pro Ala His	
375 380 385	

ctt cgc gat ggt cac tat gaa ggc gcc aaa aag ctc gga aat gca gtg 1315
 Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys Leu Gly Asn Ala Val
 390 395 400 405

gga tat tcc tat cct cac gat gat ccc agg gga gtg gtc cgg caa gaa 1363
 Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly Val Val Arg Gln Glu
 410 415 420

tat tta ccg gag aac ctg cgc gat cgg gtc tat tac gag ccc acc aca 1411
 Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr Tyr Glu Pro Thr Thr
 425 430 435

cac ggt gga gag aag cgg att gcc gag tac att ggc agg ctt cgt cgt 1459
 His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile Gly Arg Leu Arg Arg
 440 445 450

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 Ile Ile Arg Gly Thr Lys
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<210> 188

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Ala Gln Asp Ser Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala
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Gly Asn Thr Ser Ser Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe
 20 25 30

His Pro Gly Gly His Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr
 35 40 45

Leu Asp Glu Val Val Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro
 50 55 60

Leu Arg Arg Leu Ile Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr
 65 70 75 80

Gly Pro Pro Gly Thr Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala
 85 90 95

Ala Ala Gly Asp Arg Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val
 100 105 110

Lys Glu Val Arg Ala Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu
 115 120 125

Gly Gln Arg Thr Val Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys
 130 135 140

Thr Gln Gln Asp Ala Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu
 145 150 155 160

Leu Val Ala Ala Thr Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro
 165 170 175

Leu Leu Ser Arg Ser Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu

	180						185					190				
Asp	Ile	Lys 195	Thr	Val	Leu	Asn	Lys 200	Ala	Leu	Glu	Asp	Glu 205	Arg	Gly	Leu	
Ala	Gly 210	Arg	Ile	Thr	Ala	Thr 215	Asp	Glu	Ala	Val	Asp 220	Gln	Leu	Val	Leu	
Leu 225	Ala	Gly	Gly	Asp	Ala 230	Arg	Arg	Gly	Leu	Thr 235	Tyr	Ile	Glu	Ala	Ala 240	
Ala	Glu	Ala	Val	Glu 245	Asp	Gly	Gly	Val	Leu 250	Asp	Ile	Asp	Thr	Val 255	Met	
Ala	Asn	Val	Asn 260	Arg	Ala	Val	Val 265	Arg	Tyr	Asp	Arg	Asp	Gly 270	Asp	Gln	
His	Tyr	Asp 275	Val	Val	Ser	Ala	Trp 280	Ile	Lys	Ser	Ile	Arg 285	Gly	Ser	Asp	
Val	Asp 290	Ala	Ala	Leu	His	Tyr 295	Leu	Ala	Arg	Met	Ile 300	Asp	Ala	Gly	Glu	
Asp 305	Pro	Arg	Phe	Ile 310	Ala	Arg	Arg	Leu	Val	Val 315	His	Ser	Ser	Glu	Asp 320	
Ile	Gly	Met	Ala	Asp 325	Pro	Ser	Ala	Met	Gln 330	Val	Ala	Ile	Ala	Ala 335	Ala	
Gln	Ala	Val	Gln 340	Leu	Ile	Gly	Met	Pro 345	Glu	Ala	Arg	Ile	Asn 350	Leu	Ala	
Gln	Ala	Thr 355	Ile	His	Leu	Ala	Leu 360	Ala	Pro	Lys	Ser	Asn 365	Ala	Val	Ile	
Met	Ala 370	Met	Asp	Ala	Ala	Leu 375	Thr	Asp	Val	Gln	Gln 380	Gly	His	Ile	Gly	
Thr 385	Val	Pro	Ala	His 390	Leu	Arg	Asp	Gly	His	Tyr 395	Glu	Gly	Ala	Lys	Lys 400	
Leu	Gly	Asn	Ala 405	Val	Gly	Tyr	Ser	Tyr	Pro 410	His	Asp	Asp	Pro	Arg 415	Gly	
Val	Val	Arg	Gln 420	Glu	Tyr	Leu	Pro	Glu 425	Asn	Leu	Arg	Asp	Arg 430	Val	Tyr	
Tyr	Glu	Pro 435	Thr	Thr	His	Gly	Gly 440	Glu	Lys	Arg	Ile	Ala 445	Glu	Tyr	Ile	
Gly	Arg 450	Leu	Arg	Arg	Ile	Ile 455	Arg	Gly	Thr	Lys						

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<210> 189
<211> 597
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS

<222> (101)..(574)

<223> RXA00287

<400> 189

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caggaaaaat tgttgtgagg gtataaagag gacttgaaaa atg cac cat cta cgc 115
                                         Met His His Leu Arg
                                         1 5

tat gaa tca cca atc gga gag ctt ctt ctt gtt gca agt gac caa ggg 163
Tyr Glu Ser Pro Ile Gly Glu Leu Leu Leu Val Ala Ser Asp Gln Gly
                        10 15 20

cta acc tat gtg gca ttc tcc gat gaa aac tac gca gct tgt act gtc 211
Leu Thr Tyr Val Ala Phe Ser Asp Glu Asn Tyr Ala Ala Cys Thr Val
                        25 30 35

ggg tcg acc ccg gga acc aat gcg gtg ctg gaa cag gca gtt gct gag 259
Gly Ser Thr Pro Gly Thr Asn Ala Val Leu Glu Gln Ala Val Ala Glu
                        40 45 50

ctt gaa gaa tac ttc gca ggg aaa cgt aaa gag ttc agc act ccc ctg 307
Leu Glu Glu Tyr Phe Ala Gly Lys Arg Lys Glu Phe Ser Thr Pro Leu
                        55 60 65

gat tgg cca agc caa aat ctg ctg agc ttc cgc ggt aaa gtg cag gaa 355
Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg Gly Lys Val Gln Glu
                        70 75 80 85

ttt ttg ctg tcc att cct tat ggg gag agt aaa act tac aaa cag atc 403
Phe Leu Leu Ser Ile Pro Tyr Gly Glu Ser Lys Thr Tyr Lys Gln Ile
                        90 95 100

gcc gct gag ctt aat aat gtg ggc gcg gtt cgt gca gtg gga agc gcc 451
Ala Ala Glu Leu Asn Asn Val Gly Ala Val Arg Ala Val Gly Ser Ala
                        105 110 115

tgc gcc acc aac ccc ttg cca atc ttt gct cct tgt cac cga gta ctg 499
Cys Ala Thr Asn Pro Leu Pro Ile Phe Ala Pro Cys His Arg Val Leu
                        120 125 130

cgc act gat ggg gcg tta ggt ggc tac aga gga ggc ttg gaa gca aaa 547
Arg Thr Asp Gly Ala Leu Gly Gly Tyr Arg Gly Gly Leu Glu Ala Lys
                        135 140 145

cag tgg ctg ttg gag ctg gaa cgt cct tagtttgtgt ccgcgcacgg agc 597
Gln Trp Leu Leu Glu Leu Glu Arg Pro
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<210> 190

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

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Met His His Leu Arg Tyr Glu Ser Pro Ile Gly Glu Leu Leu Leu Val
  1 5 10 15

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Ala Ser Asp Gln Gly Leu Thr Tyr Val Ala Phe Ser Asp Glu Asn Tyr
 20 25 30

Ala Ala Cys Thr Val Gly Ser Thr Pro Gly Thr Asn Ala Val Leu Glu
 35 40 45

Gln Ala Val Ala Glu Leu Glu Glu Tyr Phe Ala Gly Lys Arg Lys Glu
 50 55 60

Phe Ser Thr Pro Leu Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg
 65 70 75 80

Gly Lys Val Gln Glu Phe Leu Leu Ser Ile Pro Tyr Gly Glu Ser Lys
 85 90 95

Thr Tyr Lys Gln Ile Ala Ala Glu Leu Asn Asn Val Gly Ala Val Arg
 100 105 110

Ala Val Gly Ser Ala Cys Ala Thr Asn Pro Leu Pro Ile Phe Ala Pro
 115 120 125

Cys His Arg Val Leu Arg Thr Asp Gly Ala Leu Gly Gly Tyr Arg Gly
 130 135 140

Gly Leu Glu Ala Lys Gln Trp Leu Leu Glu Leu Glu Arg Pro
 145 150 155

<210> 191

<211> 1194

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1171)

<223> RXA01687

<400> 191

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gaatctaaac tattcccaaa tagaccatac ggtctaacat gtg ttc atg ctt gca 115
 Val Phe Met Leu Ala
 1 5

cag cga aca ctc ccc att cac atc acc gcc ccc cac cta ccc gtc gcg 163
 10 15 20
 Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro His Leu Pro Val Ala

cgc gta ttt cat caa att cgc gcc aca gac gcc gat cgc acc tct ctg 211
 25 30 35
 Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala Asp Arg Thr Ser Leu

caa cgc gat ctt gaa ctc tcc caa gct ggc atc acg cgg cat gtg tca 259
 40 45 50
 Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile Thr Arg His Val Ser

gcg ctt att gat gca ggt ctc gtg gag gaa acc cga gtg gat tcc ggg 307
 55 60 65
 Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr Arg Val Asp Ser Gly

gcg cgc tcg ggg cga ccg cgc aca aaa tta ggc atc gac ggc cgc cat	355
Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly Ile Asp Gly Arg His	
70 75 80 85	
ctc acc gcc tgg gga gtg cac att ggc ctg cgc agc acg gat ttt gcg	403
Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg Ser Thr Asp Phe Ala	
90 95 100	
gtg tgc gat tta gcc ggc cga gtg att agg tat gag cgc gtg gac cat	451
Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr Glu Arg Val Asp His	
105 110 115	
gaa gtt tca cac tcc acg ccg tcg gaa acg ctg aat ttt gtc gca cat	499
Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu Asn Phe Val Ala His	
120 125 130	
agg tta caa aca ttg agc gcc ggc ttg ccc gag ccc cgc aat gtg ggc	547
Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu Pro Arg Asn Val Gly	
135 140 145	
gtg gca tta tct gcc cac tta agc gcc aac gga acc gtc act tcc gaa	595
Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly Thr Val Thr Ser Glu	
150 155 160 165	
gat tat ggc tgg tca gag gtg gaa att ggg gca cac ctc ccc ttc ccc	643
Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala His Leu Pro Phe Pro	
170 175 180	
gcc acc atc gga tca ggt gtt gcg gcg atg gcc ggt tcg gaa att atc	691
Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala Gly Ser Glu Ile Ile	
185 190 195	
aac gcg cca ctg acc caa tcc acg cag tcc acg ctg tat ttc tac gcc	739
Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr Leu Tyr Phe Tyr Ala	
200 205 210	
cgc gaa atg gtc tcc cac gcc tgg att ttc aac ggc gct gtc cac cgc	787
Arg Glu Met Val Ser His Ala Trp Ile Phe Asn Gly Ala Val His Arg	
215 220 225	
ccc aac agc ggc cgc acg ccg acg gcg ttc gga aat aca aat acc tta	835
Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly Asn Thr Asn Thr Leu	
230 235 240 245	
aaa gat gct ttt cga cgt gga ctc aca cca aca act ttc tcc gat tta	883
Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr Thr Phe Ser Asp Leu	
250 255 260	
gtc caa ctc tcc cac acc aac ccg ctt gca cga cag atc ctc aac gag	931
Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg Gln Ile Leu Asn Glu	
265 270 275	
cgc gcc cac aaa ctt gcc gac gcc gta acc acc gcc gtt gat gtt gtc	979
Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr Ala Val Asp Val Val	
280 285 290	
gac ccc gaa gcc gtc gtc ttc gcc ggc gaa gcc ttc acc ctg gat ccg	1027
Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala Phe Thr Leu Asp Pro	
295 300 305	
gaa act ctt cgc att gtg gtg acc cag ctc cga gca aac acc ggc agc	1075

Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg Ala Asn Thr Gly Ser
 310 315 320 325
 caa ctg aga atc caa cgc gca gac gcc tac att ctc cgc acc gcg gcc 1123
 Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile Leu Arg Thr Ala Ala
 330 335 340
 atc cag gtg gcg ctg cat ccg atc cgt caa gat ccg ttg gca ttt gtg 1171
 Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp Pro Leu Ala Phe Val
 345 350 355
 taattaccac ccatgttgcg ggg 1194

<210> 192
 <211> 357
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 192
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 His Leu Pro Val Ala Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala
 20 25 30
 Asp Arg Thr Ser Leu Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile
 35 40 45
 Thr Arg His Val Ser Ala Leu Ile Asp Ala Gly Leu Val Glu Glu Thr
 50 55 60
 Arg Val Asp Ser Gly Ala Arg Ser Gly Arg Pro Arg Thr Lys Leu Gly
 65 70 75 80
 Ile Asp Gly Arg His Leu Thr Ala Trp Gly Val His Ile Gly Leu Arg
 85 90 95
 Ser Thr Asp Phe Ala Val Cys Asp Leu Ala Gly Arg Val Ile Arg Tyr
 100 105 110
 Glu Arg Val Asp His Glu Val Ser His Ser Thr Pro Ser Glu Thr Leu
 115 120 125
 Asn Phe Val Ala His Arg Leu Gln Thr Leu Ser Ala Gly Leu Pro Glu
 130 135 140
 Pro Arg Asn Val Gly Val Ala Leu Ser Ala His Leu Ser Ala Asn Gly
 145 150 155 160
 Thr Val Thr Ser Glu Asp Tyr Gly Trp Ser Glu Val Glu Ile Gly Ala
 165 170 175
 His Leu Pro Phe Pro Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala
 180 185 190
 Gly Ser Glu Ile Ile Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr
 195 200 205
 Leu Tyr Phe Tyr Ala Arg Glu Met Val Ser His Ala Trp Ile Phe Asn
 210 215 220

Gly Ala Val His Arg Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly
 225 230 235 240
 Asn Thr Asn Thr Leu Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr
 245 250 255
 Thr Phe Ser Asp Leu Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg
 260 265 270
 Gln Ile Leu Asn Glu Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr
 275 280 285
 Ala Val Asp Val Val Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala
 290 295 300
 Phe Thr Leu Asp Pro Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg
 305 310 315 320
 Ala Asn Thr Gly Ser Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile
 325 330 335
 Leu Arg Thr Ala Ala Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp
 340 345 350
 Pro Leu Ala Phe Val
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<210> 193
 <211> 1287
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1264)
 <223> RXA01935

<400> 193
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 Met Ile Gly Tyr Gly
 1 5
 tta cct atg ccc aat cag gcc cac ttc tct gcg tcc ttt gcc cgc ccc 163
 Leu Pro Met Pro Asn Gln Ala His Phe Ser Ala Ser Phe Ala Arg Pro
 10 15 20
 tct acc ccg gct gca aag tgc atg cac cat atc cgc ctc ggc cag caa 211
 Ser Thr Pro Ala Ala Lys Cys Met His His Ile Arg Leu Gly Gln Gln
 25 30 35
 ctc att aga aat gag ctg gtc gag gcc aca ggt ctg tcc caa ccg act 259
 Leu Ile Arg Asn Glu Leu Val Glu Ala Thr Gly Leu Ser Gln Pro Thr
 40 45 50
 gtc acc cgc gca gtc acc gct tta atg cag gca ggt ttg gtt cgt gaa 307
 Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala Gly Leu Val Arg Glu
 55 60 65

cgc cct gat ctc aca ctc tca tgc ggc cct ggt cgt ccc aat att cct	355
Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly Arg Pro Asn Ile Pro	
70 75 80 85	
cta gaa ctc gct cca agt cca tgg att cat gca ggc gtg gca atc ggc	403
Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala Gly Val Ala Ile Gly	
90 95 100	
acc aag tct tcc tac gtc gct ttg ttt gat acc aag ggt cgc acc ctt	451
Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr Lys Gly Arg Thr Leu	
105 110 115	
cgt gat gcc atg ctg gaa atc tca gca gct gat tta gat cca gac act	499
Arg Asp Ala Met Leu Glu Ile Ser Ala Ala Asp Leu Asp Pro Asp Thr	
120 125 130	
ttc atc gaa cac ctc att gct ggt gtc aac cgc ctc acc act ggt ctt	547
Phe Ile Glu His Leu Ile Ala Gly Val Asn Arg Leu Thr Thr Gly Leu	
135 140 145	
gat cta cca ctg gta ggt att ggt gtt gcc acc tca gga aaa gtc acc	595
Asp Leu Pro Leu Val Gly Ile Gly Val Ala Thr Ser Gly Lys Val Thr	
150 155 160 165	
aac gca ggc gtt gtc acc gca agc aac ttg ggc tgg gat ggc gtt gat	643
Asn Ala Gly Val Val Thr Ala Ser Asn Leu Gly Trp Asp Gly Val Asp	
170 175 180	
atc gct ggc cgc ctg aac tac caa ttc agc gtt cca gca acc gtg gca	691
Ile Ala Gly Arg Leu Asn Tyr Gln Phe Ser Val Pro Ala Thr Val Ala	
185 190 195	
tca gca att cct gcc atc gca gct tct gaa ctg cag gct tcc cca ctt	739
Ser Ala Ile Pro Ala Ile Ala Ala Ser Glu Leu Gln Ala Ser Pro Leu	
200 205 210	
ccc cac cct gag cag cca act ccc atc acc ttg acc ttc tac gcc gat	787
Pro His Pro Glu Gln Pro Thr Pro Ile Thr Leu Thr Phe Tyr Ala Asp	
215 220 225	
gac tct gtg ggc gcg gcc tac agc aat gat ttg gga gta cat gtc att	835
Asp Ser Val Gly Ala Ala Tyr Ser Asn Asp Leu Gly Val His Val Ile	
230 235 240 245	
gga cca ctg gct aca act cgt gga tca ggt ttg gat act ttg ggc atg	883
Gly Pro Leu Ala Thr Thr Arg Gly Ser Gly Leu Asp Thr Leu Gly Met	
250 255 260	
gct gcc gaa gat gcg ctg agc acc caa ggt ttc tta agc agg gtt tct	931
Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe Leu Ser Arg Val Ser	
265 270 275	
gat cag ggt atc ttt gcc aac agc ctt ggt gag cta gtc acc att gct	979
Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu Leu Val Thr Ile Ala	
280 285 290	
aaa gac aat gaa acc gca cgg gaa ttc ctc aac gat cgc gcg acc ctg	1027
Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn Asp Arg Ala Thr Leu	
295 300 305	

ctg gct cac act gcc gca gaa gct gcc gaa aca gtt aag cca tcc acc 1075
 Leu Ala His Thr Ala Ala Glu Ala Ala Glu Thr Val Lys Pro Ser Thr
 310 315 320 325

ctg gtt ctc tcg gga tcg gcg ttt tcc gaa gat cca caa ggt cgg tcg 1123
 Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp Pro Gln Gly Arg Ser
 330 335 340

gtg ttc gct tcc caa ttg aag aag gaa tac gac gca gac att gag ctc 1171
 Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp Ala Asp Ile Glu Leu
 345 350 355

cgg ttg atc ccc acc cac cgg gaa aac gtc cgc gca gca gct cga gca 1219
 Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg Ala Ala Ala Arg Ala
 360 365 370

gtc gca ctt gat cga cta ctc aac gag cca ctt act ctc gta ccc 1264
 Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu Thr Leu Val Pro
 375 380 385

taacctcatc taagctcagt gct 1287

<210> 194
 <211> 388
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 194
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 35 40 45
 Leu Ser Gln Pro Thr Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala
 50 55 60
 Gly Leu Val Arg Glu Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly
 65 70 75 80
 Arg Pro Asn Ile Pro Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala
 85 90 95
 Gly Val Ala Ile Gly Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr
 100 105 110
 Lys Gly Arg Thr Leu Arg Asp Ala Met Leu Glu Ile Ser Ala Ala Asp
 115 120 125
 Leu Asp Pro Asp Thr Phe Ile Glu His Leu Ile Ala Gly Val Asn Arg
 130 135 140
 Leu Thr Thr Gly Leu Asp Leu Pro Leu Val Gly Ile Gly Val Ala Thr
 145 150 155 160
 Ser Gly Lys Val Thr Asn Ala Gly Val Val Thr Ala Ser Asn Leu Gly
 165 170 175

Trp Asp Gly Val Asp Ile Ala Gly Arg Leu Asn Tyr Gln Phe Ser Val
 180 185 190
 Pro Ala Thr Val Ala Ser Ala Ile Pro Ala Ile Ala Ala Ser Glu Leu
 195 200 205
 Gln Ala Ser Pro Leu Pro His Pro Glu Gln Pro Thr Pro Ile Thr Leu
 210 215 220
 Thr Phe Tyr Ala Asp Asp Ser Val Gly Ala Ala Tyr Ser Asn Asp Leu
 225 230 235 240
 Gly Val His Val Ile Gly Pro Leu Ala Thr Thr Arg Gly Ser Gly Leu
 245 250 255
 Asp Thr Leu Gly Met Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe
 260 265 270
 Leu Ser Arg Val Ser Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu
 275 280 285
 Leu Val Thr Ile Ala Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn
 290 295 300
 Asp Arg Ala Thr Leu Leu Ala His Thr Ala Ala Glu Ala Ala Glu Thr
 305 310 315 320
 Val Lys Pro Ser Thr Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp
 325 330 335
 Pro Gln Gly Arg Ser Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp
 340 345 350
 Ala Asp Ile Glu Leu Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg
 355 360 365
 Ala Ala Ala Arg Ala Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu
 370 375 380
 Thr Leu Val Pro
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<210> 195
 <211> 744
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(721)
 <223> RXN02270

<400> 195
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gcatcgctat tgggcgcggt cgtttggtgg gtggcgggtg atg gat cag gcg cgg 115
 Met Asp Gln Ala Arg
 1 5

ccg	aat	cga	acg	cac	tac	gcc	atg	gtt	gag	ctg	gag	cag	cat	ggt	ttt	163
Pro	Asn	Arg	Thr	His	Tyr	Ala	Met	Val	Glu	Leu	Glu	Gln	His	Gly	Phe	
				10					15					20		
tta	agt	ggt	gtg	gtc	acc	caa	aat	gtc	gat	ggt	tta	cac	gcg	gaa	gca	211
Leu	Ser	Gly	Val	Val	Thr	Gln	Asn	Val	Asp	Gly	Leu	His	Ala	Glu	Ala	
				25					30					35		
ggc	acg	aaa	aac	ctg	gtc	gcg	ctg	cat	ggt	gat	ctc	gcc	cat	gtg	atg	259
Gly	Thr	Lys	Asn	Leu	Val	Ala	Leu	His	Gly	Asp	Leu	Ala	His	Val	Met	
				40					45					50		
tgt	ttg	aac	tgc	ggg	ttc	ggg	gag	gat	cga	cac	ctc	ttt	gat	gaa	cgt	307
Cys	Leu	Asn	Cys	Gly	Phe	Gly	Glu	Asp	Arg	His	Leu	Phe	Asp	Glu	Arg	
				55					60					65		
ctc	gaa	gcc	gcc	aac	ccc	ggc	tac	gtc	gct	tcc	att	cgc	ctg	gaa	ccg	355
Leu	Glu	Ala	Ala	Asn	Pro	Gly	Tyr	Val	Ala	Ser	Ile	Arg	Leu	Glu	Pro	
				70					75					80		
ggc	gca	gtc	aac	ccc	gac	ggc	gac	gtc	ttc	ctc	gac	gaa	gaa	caa	gta	403
Gly	Ala	Val	Asn	Pro	Asp	Gly	Asp	Val	Phe	Leu	Asp	Glu	Glu	Gln	Val	
				90					95					100		
cgc	cgc	ttc	acc	atg	atc	ggc	tgc	ttg	cgc	tgc	ggc	tgc	ctc	atg	ctc	451
Arg	Arg	Phe	Thr	Met	Ile	Gly	Cys	Leu	Arg	Cys	Gly	Ser	Leu	Met	Leu	
				105					110					115		
aaa	cca	gac	gtg	gtt	tac	ttc	ggc	gaa	ccc	gtg	ccc	gcc	gcg	cgc	aaa	499
Lys	Pro	Asp	Val	Val	Tyr	Phe	Gly	Glu	Pro	Val	Pro	Ala	Ala	Arg	Lys	
				120					125					130		
aaa	gat	tta	aaa	aag	ctt	ctc	gac	gcc	tcc	tcc	agc	ctc	tta	atc	gcc	547
Lys	Asp	Leu	Lys	Lys	Leu	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Leu	Ile	Ala	
				135					140					145		
ggc	tcc	tcc	cta	gcc	gtc	atg	agt	gga	tac	cgg	atc	gtc	atc	gaa	gcg	595
Gly	Ser	Ser	Leu	Ala	Val	Met	Ser	Gly	Tyr	Arg	Ile	Val	Ile	Glu	Ala	
				150					155					160		
caa	cgt	caa	gga	aaa	caa	gtg	tct	gtc	atc	aac	ggc	ggc	cca	ggt	cgg	643
Gln	Arg	Gln	Gly	Lys	Gln	Val	Ser	Val	Ile	Asn	Gly	Gly	Pro	Gly	Arg	
				170					175					180		
gcg	gat	tcc	cgc	gtg	gac	att	ttg	tgg	cgc	acc	cgc	ggt	gca	ccg	gcc	691
Ala	Asp	Ser	Arg	Val	Asp	Ile	Leu	Trp	Arg	Thr	Arg	Val	Ala	Pro	Ala	
				185					190					195		
ttt	gat	gac	att	ttg	gac	gcg	ctg	gac	ctt	tagactttttg	gtggcettaag	ttc				744
Phe	Asp	Asp	Ile	Leu	Asp	Ala	Leu	Asp	Leu							
				200					205							

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<212> PRT
<213> Corynebacterium glutamicum
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Glu Gln His Gly Phe Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly
 20 25 30
 Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp
 35 40 45
 Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
 50 55 60
 Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
 65 70 75 80
 Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
 85 90 95
 Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
 100 105 110
 Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
 115 120 125
 Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
 130 135 140
 Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
 145 150 155 160
 Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn
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 180 185 190
 Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
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<210> 197

<211> 744

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(721)

<223> FRXA02270

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gcacgcgtat tgggcgcggt cgtttgtggg gtggcgggtg atg gat cag gcg cgg 115
 Met Asp Gln Ala Arg
 1 5

ccg aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt 163
 Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe
 10 15 20

tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca 211
 Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala

25										30					35					
ggc	acg	aaa	aac	ctg	gtc	gcg	ctg	cat	ggt	gat	ctc	gcc	cat	gtg	atg	259				
Gly	Thr	Lys	Asn	Leu	Val	Ala	Leu	His	Gly	Asp	Leu	Ala	His	Val	Met					
		40					45					50								
tgt	ttg	aac	tgc	ggt	ttc	ggg	gag	gat	cga	cac	ctc	ttt	gat	gaa	cgt	307				
Cys	Leu	Asn	Cys	Gly	Phe	Gly	Glu	Asp	Arg	His	Leu	Phe	Asp	Glu	Arg					
	55					60					65									
ctc	gaa	gcc	gcc	aac	ccc	ggc	tac	gtc	gct	tcc	att	cgc	ctg	gaa	ccg	355				
Leu	Glu	Ala	Ala	Asn	Pro	Gly	Tyr	Val	Ala	Ser	Ile	Arg	Leu	Glu	Pro					
	70				75					80					85					
ggc	gca	gtc	aac	ccc	gac	ggc	gac	gtc	ttc	ctc	gac	gaa	gaa	caa	gta	403				
Gly	Ala	Val	Asn	Pro	Asp	Gly	Asp	Val	Phe	Leu	Asp	Glu	Glu	Gln	Val					
				90					95					100						
cgc	cgc	ttc	acc	atg	atc	ggc	tgc	ttg	cgc	tgc	ggc	tcg	ctc	atg	ctc	451				
Arg	Arg	Phe	Thr	Met	Ile	Gly	Cys	Leu	Arg	Cys	Gly	Ser	Leu	Met	Leu					
			105				110						115							
aaa	cca	gac	gtg	gtt	tac	ttc	ggc	gaa	ccc	gtg	ccc	gcc	gcg	cgc	aaa	499				
Lys	Pro	Asp	Val	Val	Tyr	Phe	Gly	Glu	Pro	Val	Pro	Ala	Ala	Arg	Lys					
		120					125					130								
aaa	gat	tta	aaa	aag	ctt	ctc	gac	gcc	tcc	tcc	agc	ctc	tta	atc	gcc	547				
Lys	Asp	Leu	Lys	Lys	Leu	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Leu	Ile	Ala					
	135					140					145									
ggc	tcc	tcc	cta	gcc	gtc	atg	agt	gga	tac	cgg	atc	gtc	atc	gaa	gcg	595				
Gly	Ser	Ser	Leu	Ala	Val	Met	Ser	Gly	Tyr	Arg	Ile	Val	Ile	Glu	Ala					
	150				155					160					165					
caa	cgt	caa	gga	aaa	caa	gtg	tct	gtc	atc	aac	ggc	ggc	cca	ggg	cgg	643				
Gln	Arg	Gln	Gly	Lys	Gln	Val	Ser	Val	Ile	Asn	Gly	Gly	Pro	Gly	Arg					
				170					175					180						
gcg	gat	tcc	cgc	gtg	gac	att	ttg	tgg	cgc	acc	cgc	gtt	gca	ccg	gcc	691				
Ala	Asp	Ser	Arg	Val	Asp	Ile	Leu	Trp	Arg	Thr	Arg	Val	Ala	Pro	Ala					
			185					190					195							
ttt	gat	gac	att	ttg	gac	gcg	ctg	gac	ctt	tagacttttg gtggcttaag ttc						744				
Phe	Asp	Asp	Ile	Leu	Asp	Ala	Leu	Asp	Leu											
		200					205													

<210> 198

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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Glu	Gln	His	Gly	Phe	Leu	Ser	Gly	Val	Val	Thr	Gln	Asn	Val	Asp	Gly
			20					25					30		

Leu	His	Ala	Glu	Ala	Gly	Thr	Lys	Asn	Leu	Val	Ala	Leu	His	Gly	Asp
		35					40					45			

Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
 50 55 60
 Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
 65 70 75 80
 Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
 85 90 95
 Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
 100 105 110
 Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
 115 120 125
 Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
 130 135 140
 Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
 145 150 155 160
 Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn
 165 170 175
 Gly Gly Pro Gly Arg Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr
 180 185 190
 Arg Val Ala Pro Ala Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
 195 200 205

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(580)
 <223> RXA01241

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 aagggttcc tgcgcatggg accctaataa gcctcgcgcg gtg gat gtt cgc cac 115
 Val Asp Val Arg His
 1 5
 ctt cca gaa act gaa agc cgt tcc tcc aag gct gct aca cag gca aag 163
 Leu Pro Glu Thr Glu Ser Arg Ser Ser Lys Ala Ala Thr Gln Ala Lys
 10 15 20
 agc aag gcc cct cag gcc ggg gtc cat gat cct gag tta gct ggc cag 211
 Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro Glu Leu Ala Gly Gln
 25 30 35
 acc tca ttt gtc cca gtg gtg ggc aaa att gcc gct ggt agc ccg atc 259
 Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala Ala Gly Ser Pro Ile
 40 45 50

acc gct gag cag aac atc gaa gag tac tac cca ctc ccc gca gaa atc 307
 Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro Leu Pro Ala Glu Ile
 55 60 65

gtc gga gac ggt gac ttg ttc atg ctc cag gtt gtt ggc gag tcc atg 355
 Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val Val Gly Glu Ser Met
 70 75 80 85

agg gat gct ggc atc ctc acc ggc gac tgg gtt gtt gtt cgt tcc cag 403
 Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val Val Val Arg Ser Gln
 90 95 100

ccg gta gct gag cag ggc gag ttc gtc gcg gca atg att gac ggt gaa 451
 Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala Met Ile Asp Gly Glu
 105 110 115

gcc acc gtg aag gaa ttc cac aag gat tca tct ggc atc tgg ctc ctg 499
 Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser Gly Ile Trp Leu Leu
 120 125 130

cca cac aac gat acg ttt gcc cca att cct gct gag aat gca gaa atc 547
 Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala Glu Asn Ala Glu Ile
 135 140 145

atg ggc aag gtt gtt tcc gtg atg cgc aag ctt taagtcgctt ttcagggttcc 600
 Met Gly Lys Val Val Ser Val Met Arg Lys Leu
 150 155 160

cgc 603

<210> 200

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Val Asp Val Arg His Leu Pro Glu Thr Glu Ser Arg Ser Ser Lys Ala
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Ala Thr Gln Ala Lys Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro
 20 25 30

Glu Leu Ala Gly Gln Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala
 35 40 45

Ala Gly Ser Pro Ile Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro
 50 55 60

Leu Pro Ala Glu Ile Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val
 65 70 75 80

Val Gly Glu Ser Met Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val
 85 90 95

Val Val Arg Ser Gln Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala
 100 105 110

Met Ile Asp Gly Glu Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser
 115 120 125

Gly Ile Trp Leu Leu Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala
130 135 140

Glu Asn Ala Glu Ile Met Gly Lys Val Val Ser Val Met Arg Lys Leu
145 150 155 160

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<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(754)

<223> RXA02127

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tgagggaaca tcccaaacc aaagaaccta ggagaacatt atg agt gag aca gtt 115
Met Ser Glu Thr Val
1 5

tta gtc ata gga gca aca gga agc ata ggc cga cat gtt gtc tcg gaa 163
Leu Val Ile Gly Ala Thr Gly Ser Ile Gly Arg His Val Val Ser Glu
10 15 20

gca ctt aac cag gga tac caa gtt aag gca ttt gtc cgt agc aag tcc 211
Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe Val Arg Ser Lys Ser
25 30 35

cgt gca cgg gtg ctt cca gct gag gca gag att atc gta gga gac ctg 259
Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile Ile Val Gly Asp Leu
40 45 50

ctt gat cct tcc tcg att gag aaa gct gta aaa ggc gtc gag gga atc 307
Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys Gly Val Glu Gly Ile
55 60 65

att ttc act cac ggc acc tcc act cgt aaa agc gat gtg cgg gat gtt 355
Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser Asp Val Arg Asp Val
70 75 80 85

gat tac acc ggc gtt gcc aac acg ttg aag gca gtc aag gga aaa gat 403
Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala Val Lys Gly Lys Asp
90 95 100

gta aaa att gtg ctg atg acc gcc gtt gga acg acc cgc cca ggt gtg 451
Val Lys Ile Val Leu Met Thr Ala Val Gly Thr Thr Arg Pro Gly Val
105 110 115

gct tat gcc gag tgg aag cga cat ggc gag caa ctt gtt cga gct agc 499
Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln Leu Val Arg Ala Ser
120 125 130

gga cac ggt tac acc att gtt cgc cct ggt tgg ttt gat tac aac aac 547
Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp Phe Asp Tyr Asn Asn
135 140 145

gat gac gag cgt cag atc gtc atg ctt caa ggc gac acc aat cag tcg 595

Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly Asp Thr Asn Gln Ser
 150 155 160 165
 ggt ggc cca gcc gat ggc gtg att gcg cgt gat caa atc gcg cga gtt 643
 Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp Gln Ile Ala Arg Val
 170 175 180
 ttg gtt agc agt ttg aat gat gca aaa gca cga aac aaa acc ttc gag 691
 Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg Asn Lys Thr Phe Glu
 185 190 195
 ctt tct gcc act tat gga cct gcc caa gga aag cct gac cgc aac ttt 739
 Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys Pro Asp Arg Asn Phe
 200 205 210
 tgc agc act tcg ggc tgacgatacc gatgatattg acg 777
 Cys Ser Thr Ser Gly
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<210> 202

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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 His Val Val Ser Glu Ala Leu Asn Gln Gly Tyr Gln Val Lys Ala Phe
 20 25 30
 Val Arg Ser Lys Ser Arg Ala Arg Val Leu Pro Ala Glu Ala Glu Ile
 35 40 45
 Ile Val Gly Asp Leu Leu Asp Pro Ser Ser Ile Glu Lys Ala Val Lys
 50 55 60
 Gly Val Glu Gly Ile Ile Phe Thr His Gly Thr Ser Thr Arg Lys Ser
 65 70 75 80
 Asp Val Arg Asp Val Asp Tyr Thr Gly Val Ala Asn Thr Leu Lys Ala
 85 90 95
 Val Lys Gly Lys Asp Val Lys Ile Val Leu Met Thr Ala Val Gly Thr
 100 105 110
 Thr Arg Pro Gly Val Ala Tyr Ala Glu Trp Lys Arg His Gly Glu Gln
 115 120 125
 Leu Val Arg Ala Ser Gly His Gly Tyr Thr Ile Val Arg Pro Gly Trp
 130 135 140
 Phe Asp Tyr Asn Asn Asp Asp Glu Arg Gln Ile Val Met Leu Gln Gly
 145 150 155 160
 Asp Thr Asn Gln Ser Gly Gly Pro Ala Asp Gly Val Ile Ala Arg Asp
 165 170 175
 Gln Ile Ala Arg Val Leu Val Ser Ser Leu Asn Asp Ala Lys Ala Arg
 180 185 190

Asn Lys Thr Phe Glu Leu Ser Ala Thr Tyr Gly Pro Ala Gln Gly Lys
 195 200 205

Pro Asp Arg Asn Phe Cys Ser Thr Ser Gly
 210 215

<210> 203

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(838)

<223> RXA00583

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actgttaaata gtgttaaacc tgcccagact gctgtaccgc gtg tat gag cgc cgt 115
 Val Tyr Glu Arg Arg
 1 5

ctt tta aga gaa cta gac ggc gcc aaa cag ccc ggt cac gtt gcc atc 163
 Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro Gly His Val Ala Ile
 10 15 20

atg tgt gat ggc aac cga cgc tgg gcc cgg gaa gcg ggc ttc act gat 211
 Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu Ala Gly Phe Thr Asp
 25 30 35

gtc agc cat ggg cac cga gtg ggt gcc aaa aag atc ggc gag atg gtc 259
 Val Ser His Gly His Arg Val Gly Ala Lys Lys Ile Gly Glu Met Val
 40 45 50

cgc tgg tgt gat gat gta gac gtc aat ctc gtg acc gtt tat ttg ctg 307
 Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val Thr Val Tyr Leu Leu
 55 60 65

tct atg gaa aac ctt ggg cga tcc tcc gaa gag ctg caa ttg ctg ttc 355
 Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu Leu Gln Leu Leu Phe
 70 75 80 85

gat atc atc gcc gat gtc gct gat gaa ctc gcg cgt cct gaa acc aac 403
 Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala Arg Pro Glu Thr Asn
 90 95 100

tgt cga gtc cgc ctc gtt ggt cat tta gat ctg ctc cca gac cca gtt 451
 Cys Arg Val Arg Leu Val Gly His Leu Asp Leu Leu Pro Asp Pro Val
 105 110 115

gct tgt cgt tta cgc aaa gct gaa gaa gct acc gtt aac aac aca ggc 499
 Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr Val Asn Asn Thr Gly
 120 125 130

atc gca gtc aac atg gct gtc ggt tat ggc gga cgc cag gaa atc gtt 547
 Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly Arg Gln Glu Ile Val
 135 140 145

gat gcc gtg caa aaa ctt ctg acc atc ggc aag gac gag ggc cta agc 595
Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys Asp Glu Gly Leu Ser 165
150 155 160

gtt gat gaa ctg atc gaa tcc gtc aag gta gat gcg atc tcc act cac 643
Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp Ala Ile Ser Thr His 180
170 175

ctg tac acc tct ggc caa cca gac cca gac ctg gtg atc cgc acc tct 691
Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu Val Ile Arg Thr Ser 195
185 190

ggg gag cag cga ctt tcc gga ttc atg ctg tgg caa tct gcc tac tcc 739
Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp Gln Ser Ala Tyr Ser 210
200 205

gaa atc tgg ttc aca gac acc tac tgg cca gcc ttc cga cgc atc gac 787
Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala Phe Arg Arg Ile Asp 225
215 220

ttc ctc cgc gcc att cgc gac tac tcg cag cgc agc aga aga ttc ggt 835
Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg Ser Arg Arg Phe Gly 245
230 235 240

aaa taacttattc tccaaggaga gac 861
Lys

<210> 204

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Val Tyr Glu Arg Arg Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro 15
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Gly His Val Ala Ile Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu 30
20 25

Ala Gly Phe Thr Asp Val Ser His Gly His Arg Val Gly Ala Lys Lys 45
35 40

Ile Gly Glu Met Val Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val 60
50 55

Thr Val Tyr Leu Leu Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu 80
65 70 75

Leu Gln Leu Leu Phe Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala 95
85 90

Arg Pro Glu Thr Asn Cys Arg Val Arg Leu Val Gly His Leu Asp Leu 110
100 105

Leu Pro Asp Pro Val Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr 125
115 120

Val Asn Asn Thr Gly Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly 140
130 135

Arg Gln Glu Ile Val Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys
 145 150 155 160
 Asp Glu Gly Leu Ser Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp
 165 170 175
 Ala Ile Ser Thr His Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu
 180 185 190
 Val Ile Arg Thr Ser Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp
 195 200 205
 Gln Ser Ala Tyr Ser Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala
 210 215 220
 Phe Arg Arg Ile Asp Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg
 225 230 235 240
 Ser Arg Arg Phe Gly Lys
 245

<210> 205
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(559)
 <223> RXA00592

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 acctcgttgc ttacatgaag cgtgaggtgg cttagttctt atg gct tct aat tcc 115
 Met Ala Ser Asn Ser
 1 5
 gaa cgc ctt gca gag ctg ggc att tct ctt cct tcc gtt gca gcg cct 163
 Glu Arg Leu Ala Glu Leu Gly Ile Ser Leu Pro Ser Val Ala Ala Pro
 10 15 20
 gtt gct gcg tat gtt cct gcg att cag acc ggt aac cag gtg tgg act 211
 Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly Asn Gln Val Trp Thr
 25 30 35
 tct ggt cag ctg cct ttc gtt gat ggt cag ctt ccg gcc acc ggc aag 259
 Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu Pro Ala Thr Gly Lys
 40 45 50
 gtt ggc gct gag gtt tcc gct gag gat gcg gag aag ttg gct cgt gcg 307
 Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu Lys Leu Ala Arg Ala
 55 60 65
 gct gcg cta aac gct ctt gct gcg att gat gcg ctt gtt ggc att gat 355
 Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala Leu Val Gly Ile Asp
 70 75 80 85
 aag gtc act cgc gtt ttg aag att gtt ggt ttc gtg gcg tct gct gat 403

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<210> 206
<211> 153
<212> PRT
<213> Corynebacterium glutamicum
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<210> 207
<211> 182
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (1)..(159)

<223> RXA00630

<400> 207

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Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
  1             5             10             15

aac gtc gtg gaa tcc tac atc tcc tac ctg cgc cgc aag gtg gac acc   96
Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
             20             25             30

cag gat ccg cag cta att cag act gtt cgt ggc gtt gga tat gtt ctg   144
Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
             35             40             45

cgc acc cca cgt agc taaattctcc tatggaaaat cct   182
Arg Thr Pro Arg Ser
             50

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<210> 208

<211> 53

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

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Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
  1             5             10             15

Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
             20             25             30

Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
             35             40             45

Arg Thr Pro Arg Ser
             50

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<210> 209

<211> 484

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(484)

<223> FRXA00638

<400> 209

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ttcactagtg ggaagttaat cattccgcta atggacacca atg gaa gag ata aaa   115
                               Met Glu Glu Ile Lys
                               1             5

atg gac aac cag tct gac gga caa atc cgc gta ctc gtc gtt gat gac   163

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Met  Asp  Asn  Gln  Ser  Asp  Gly  Gln  Ile  Arg  Val  Leu  Val  Val  Asp  Asp
      10                      15                      20

gag  cca  aac  atc  gtc  gag  ctg  ctc  acc  gta  agc  ctt  aaa  ttc  caa  ggc  211
Glu  Pro  Asn  Ile  Val  Glu  Leu  Leu  Thr  Val  Ser  Leu  Lys  Phe  Gln  Gly
      25                      30                      35

ttc  gca  gtg  atg  acc  gcc  aac  gat  ggc  aat  gaa  gcc  ctg  aag  att  gct  259
Phe  Ala  Val  Met  Thr  Ala  Asn  Asp  Gly  Asn  Glu  Ala  Leu  Lys  Ile  Ala
      40                      45                      50

cgt  gag  ttc  cgt  cca  gac  gca  tac  atc  ctc  gat  gtc  atg  atg  cca  gga  307
Arg  Glu  Phe  Arg  Pro  Asp  Ala  Tyr  Ile  Leu  Asp  Val  Met  Met  Pro  Gly
      55                      60                      65

atg  gac  ggc  ttc  gag  ctg  ctg  acc  aag  ctg  cgc  ggc  gaa  ggc  ctt  gac  355
Met  Asp  Gly  Phe  Glu  Leu  Leu  Thr  Lys  Leu  Arg  Gly  Glu  Gly  Leu  Asp
      70                      75                      80                      85

agc  cca  gtt  ctg  tac  ctc  acc  gca  aag  gat  gcc  gtg  gag  cac  cgc  atc  403
Ser  Pro  Val  Leu  Tyr  Leu  Thr  Ala  Lys  Asp  Ala  Val  Glu  His  Arg  Ile
      90                      95                      100

cac  ggc  ctg  acc  atc  ggc  gct  gac  gac  tac  gtg  acc  aag  cct  ttc  tcc  451
His  Gly  Leu  Thr  Ile  Gly  Ala  Asp  Asp  Tyr  Val  Thr  Lys  Pro  Phe  Ser
      105                      110                      115

ctg  gaa  gaa  gta  atc  acc  cgc  ctg  cgc  gtg  att  484
Leu  Glu  Glu  Val  Ile  Thr  Arg  Leu  Arg  Val  Ile
      120                      125

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<211> 128

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

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Leu  Val  Val  Asp  Asp  Glu  Pro  Asn  Ile  Val  Glu  Leu  Leu  Thr  Val  Ser
      20                      25                      30

Leu  Lys  Phe  Gln  Gly  Phe  Ala  Val  Met  Thr  Ala  Asn  Asp  Gly  Asn  Glu
      35                      40                      45

Ala  Leu  Lys  Ile  Ala  Arg  Glu  Phe  Arg  Pro  Asp  Ala  Tyr  Ile  Leu  Asp
      50                      55                      60

Val  Met  Met  Pro  Gly  Met  Asp  Gly  Phe  Glu  Leu  Leu  Thr  Lys  Leu  Arg
      65                      70                      75                      80

Gly  Glu  Gly  Leu  Asp  Ser  Pro  Val  Leu  Tyr  Leu  Thr  Ala  Lys  Asp  Ala
      85                      90                      95

Val  Glu  His  Arg  Ile  His  Gly  Leu  Thr  Ile  Gly  Ala  Asp  Asp  Tyr  Val
      100                      105                      110

Thr  Lys  Pro  Phe  Ser  Leu  Glu  Glu  Val  Ile  Thr  Arg  Leu  Arg  Val  Ile
      115                      120                      125

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<223> RXA00894
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aactagtcgt aattagtcgg attttaagga ggctcacgcc atg ggc att gag ttt 115																
Met Gly Ile Glu Phe 5																
aag cgt tca ccg cga ccc acc ctg ggc gtt gag tgg gaa att gca ctt 163																
Lys Arg Ser Pro Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu 20																
gtt gat cca gaa aca cgt gat cta gcc ccg cgc gct gca gaa ata cta 211																
Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg Ala Ala Glu Ile Leu 35																
gag att gtg gcc aag aac cac cct gag gtg cac ctc gag cgc gaa ttc 259																
Glu Ile Val Ala Lys Asn His Pro Glu Val His Leu Glu Arg Glu Phe 50																
ctc caa aac acc gtg gag ctt gtc acc gga gtg tgc gac acc gtc ccc 307																
Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val Cys Asp Thr Val Pro 65																
gaa gcg gtg gca gag ctt tcc cac gat cta gat gcg ctg aaa gaa gca 355																
Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp Ala Leu Lys Glu Ala 85																
gcg gat tct ctc ggg ctt cgg ttg tgg acc tct gga tcc cac cca ttt 403																
Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser Gly Ser His Pro Phe 100																
tcg gat ttc cgc gaa aac cca gta tct gaa aaa ggc tcc tac gac gag 451																
Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys Gly Ser Tyr Asp Glu 115																
atc atc gcg cgc acc caa tac tgg gga aac cag atg ttg att tgg ggc 499																
Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln Met Leu Ile Trp Gly 130																
att cac gtc cac gtg ggc atc agc cat gaa gat cgc gtg tgg ccg atc 547																
Ile His Val His Val Gly Ile Ser His Glu Asp Arg Val Trp Pro Ile 145																
atc aat gcg ctg ctg aca aat tac cca cat ctg ttg gca ctt tct gca 595																
Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu Leu Ala Leu Ser Ala 165																
agc tct ccagca tgg gac gga ctt gat acc ggt tat gcc tcc aac cgg 643																
Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly Tyr Ala Ser Asn Arg																

170	175	180	
acg atg ctc tac caa cag ctg cct	aca gcc gga ctg cca tac caa ttc	691	
Thr Met Leu Tyr Gln Gln Leu Pro	Thr Ala Gly Leu Pro Tyr Gln Phe		
185	190	195	
caa agc tgg gat gaa tgg tgc agc	tac atg gcg gat caa gat aaa tcc	739	
Gln Ser Trp Asp Glu Trp Cys Ser	Tyr Met Ala Asp Gln Asp Lys Ser		
200	205	210	
ggt gtc atc aac cac acc gga tcc	atg cac ttt gat atc cgc ccc gca	787	
Gly Val Ile Asn His Thr Gly Ser	Met His Phe Asp Ile Arg Pro Ala		
215	220	225	
tcc aaa tgg gga acc atc gaa gtc	cgc gtg gcc gat tct acc tcc aac	835	
Ser Lys Trp Gly Thr Ile Glu Val	Arg Val Ala Asp Ser Thr Ser Asn		
230	235	240	
ctg cgg gaa ctg tct gcc atc gtg	gcg ttg acc cac tgt ctc gtg gtg	883	
Leu Arg Glu Leu Ser Ala Ile Val	Ala Leu Thr His Cys Leu Val Val		
250	255	260	
cac tac gac cgc atg atc gac gct	ggc gaa gag ctt ccc tcc ctg caa	931	
His Tyr Asp Arg Met Ile Asp Ala	Gly Glu Glu Leu Pro Ser Leu Gln		
265	270	275	
caa tgg cac gtt tgc gaa aat aaa	tgg cgc gcg gct agg tat ggt ctg	979	
Gln Trp His Val Ser Glu Asn Lys	Trp Arg Ala Ala Arg Tyr Gly Leu		
280	285	290	
gat gcc gaa atc atc att tcc aga	gac acc gat gaa gcg atg gtt caa	1027	
Asp Ala Glu Ile Ile Ile Ser Arg	Asp Thr Asp Glu Ala Met Val Gln		
295	300	305	
gac gaa ctc cgc cga cta gta gcg	caa ttg atg cct cta gcc aac gaa	1075	
Asp Glu Leu Arg Arg Leu Val Ala	Gln Leu Met Pro Leu Ala Asn Glu		
310	315	320	
ctc ggc tgc gct cgt gag ctt gaa	ctt gtg ttg gaa atc ctg gaa cgt	1123	
Leu Gly Cys Ala Arg Glu Leu Glu	Leu Val Leu Glu Ile Leu Glu Arg		
330	335	340	
ggt ggt gga tac gaa cgc caa cgc	aga gtg ttt aaa gaa act ggc agt	1171	
Gly Gly Gly Tyr Glu Arg Gln Arg	Arg Val Phe Lys Glu Thr Gly Ser		
345	350	355	
tgg aaa gct gca gtt gat tta gcc	tgc gac gaa ctc aac gac ctc aaa	1219	
Trp Lys Ala Ala Val Asp Leu Ala	Cys Asp Glu Leu Asn Asp Leu Lys		
360	365	370	
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Ala Leu Asp			
375			

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<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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 Trp Glu Ile Ala Leu Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg
 20 25 30
 Ala Ala Glu Ile Leu Glu Ile Val Ala Lys Asn His Pro Glu Val His
 35 40 45
 Leu Glu Arg Glu Phe Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val
 50 55 60
 Cys Asp Thr Val Pro Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp
 65 70 75 80
 Ala Leu Lys Glu Ala Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser
 85 90 95
 Gly Ser His Pro Phe Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys
 100 105 110
 Gly Ser Tyr Asp Glu Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln
 115 120 125
 Met Leu Ile Trp Gly Ile His Val His Val Gly Ile Ser His Glu Asp
 130 135 140
 Arg Val Trp Pro Ile Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu
 145 150 155 160
 Leu Ala Leu Ser Ala Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly
 165 170 175
 Tyr Ala Ser Asn Arg Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly
 180 185 190
 Leu Pro Tyr Gln Phe Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala
 195 200 205
 Asp Gln Asp Lys Ser Gly Val Ile Asn His Thr Gly Ser Met His Phe
 210 215 220
 Asp Ile Arg Pro Ala Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala
 225 230 235 240
 Asp Ser Thr Ser Asn Leu Arg Glu Leu Ser Ala Ile Val Ala Leu Thr
 245 250 255
 His Cys Leu Val Val His Tyr Asp Arg Met Ile Asp Ala Gly Glu Glu
 260 265 270
 Leu Pro Ser Leu Gln Gln Trp His Val Ser Glu Asn Lys Trp Arg Ala
 275 280 285
 Ala Arg Tyr Gly Leu Asp Ala Glu Ile Ile Ile Ser Arg Asp Thr Asp
 290 295 300
 Glu Ala Met Val Gln Asp Glu Leu Arg Arg Leu Val Ala Gln Leu Met
 305 310 315 320
 Pro Leu Ala Asn Glu Leu Gly Cys Ala Arg Glu Leu Glu Leu Val Leu

	325		330		335
Glu Ile Leu	Glu Arg Gly Gly Gly Tyr	Glu Arg Gln Arg Arg Val Phe			
	340	345		350	
Lys Glu Thr	Gly Ser Trp Lys Ala Ala Val Asp Leu	Ala Cys Asp Glu			
	355	360	365		
Leu Asn Asp	Leu Lys Ala Leu Asp				
370	375				

<210> 213
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(664)
 <223> RXA01450

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 Val Pro Val Thr Leu
 1 5
 act ctt gga atc gtc ggc ctg ccc aac gtt ggc aag tcc acc ctg ttc 163
 Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser Thr Leu Phe
 10 15 20
 aac gcc ctg act cgc aat gac gtg ctc gca gcg aac tac ccg ttc gcc 211
 Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala Asn Tyr Pro Phe Ala
 25 30 35
 acc atc gag cca aac gtg ggc ctt gtc gag ctt cca gac gct cgc ctt 259
 Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu Pro Asp Ala Arg Leu
 40 45 50
 gaa cgc ctt tct gaa atc ttc ggc tct gag cgc atc ctg cca gca acc 307
 Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg Ile Leu Pro Ala Thr
 55 60 65
 gtg tct ttc gtt gac atc gcc gga atc gtt aag gga gct tcc gaa ggc 355
 Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys Gly Ala Ser Glu Gly
 70 75 80 85
 gaa gga atg ggc aac gct ttc ctt gcc aac atc cgc gaa gca gac gct 403
 Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile Arg Glu Ala Asp Ala
 90 95 100
 atc tgt cag gtt gtg cgc gca ttc gct gac gaa aac gtc att cac gtc 451
 Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu Asn Val Ile His Val
 105 110 115
 gat ggt gaa gtt aac cca gca acc gat atc tct gtg atc aac acc gag 499
 Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser Val Ile Asn Thr Glu
 120 125 130

ctg atc ctc gcc gac ctg cag acc gtg gaa aaa gca ctc cca cgc ctc 547
 Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys Ala Leu Pro Arg Leu
 135 140 145

gaa aag gat gca cgc aaa gac aag gga ctt ggc gaa gtc gta gat gag 595
 Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly Glu Val Val Asp Glu
 150 155 160 165

acc aaa aaa gcc ctt gcg atc ttg agc gat gac cgc acc ttg ttt ctc 643
 Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp Arg Thr Leu Phe Leu
 170 175 180

tgc agc aaa agc tgg cga cat tgatctggcc ctcctgcgcg atc 687
 Cys Ser Lys Ser Trp Arg His
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<210> 214

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

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Lys Ser Thr Leu Phe Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala
 20 25 30

Asn Tyr Pro Phe Ala Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu
 35 40 45

Pro Asp Ala Arg Leu Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg
 50 55 60

Ile Leu Pro Ala Thr Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys
 65 70 75 80

Gly Ala Ser Glu Gly Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile
 85 90 95

Arg Glu Ala Asp Ala Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu
 100 105 110

Asn Val Ile His Val Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser
 115 120 125

Val Ile Asn Thr Glu Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys
 130 135 140

Ala Leu Pro Arg Leu Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly
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Glu Val Val Asp Glu Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp
 165 170 175

Arg Thr Leu Phe Leu Cys Ser Lys Ser Trp Arg His
 180 185

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 <222> (101)..(667)
 <223> RXA01451

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gtcgtagatg agaccaaaaa agcccttgcg atcttgagcg atg acc gca cct tgt 115
                               Met Thr Ala Pro Cys
                               1           5

ttc tct gca gca aaa gct ggc gac att gat ctg gcc ctc ctg cgc gat 163
Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu Ala Leu Leu Arg Asp
                               10           15           20

ctc cac ctg atg aca gca aag cct ttc ctc tac gtc ttc aac tcc gac 211
Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr Val Phe Asn Ser Asp
                               25           30           35

gaa aaa gtg ctc acc gac gac gcc aag aag gac gaa ctc cgc gca cta 259
Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp Glu Leu Arg Ala Leu
                               40           45           50

gtc gcg cca gca gac tgc gta ttc ctt gac gca caa act gaa acc gaa 307
Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala Gln Thr Glu Thr Glu
                               55           60           65

ctt ctt gaa ctc gaa gaa gac gaa gca gca gaa ctc ctc gaa gct gta 355
Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu Leu Leu Glu Ala Val
                               70           75           80           85

ggc caa acg gaa cca ggc cta cac tcc ctc gca cgt gca gga ttt gaa 403
Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala Arg Ala Gly Phe Glu
                               90           95           100

acc ctc gga cta cag acc tac ctc acc gcg ggt cct aag gaa tca cgc 451
Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly Pro Lys Glu Ser Arg
                               105           110           115

gcc tgg acc atc cac aag ggc gac acc gct cca cag gca gca ggc gtt 499
Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro Gln Ala Ala Gly Val
                               120           125           130

atc cat tct gac ttc gaa cgc ggc ttc atc aag gct gaa atc gtc tcc 547
Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys Ala Glu Ile Val Ser
                               135           140           145

ttc gaa gat ctt gac gct gct ggt tcc atg gcg gaa gcc aag gcc cag 595
Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala Glu Ala Lys Ala Gln
                               150           155           160           165

ggc aaa gtc cgc caa gaa ggt aag gac tac gtg atg gtc gat ggc gac 643
Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val Met Val Asp Gly Asp
                               170           175           180

gtt gtg gag ttc cgg ttt aac gtc tagcggttatt gacgctcctc gtt 690
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185

<210> 216

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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20 25 30

Val Phe Asn Ser Asp Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp
35 40 45

Glu Leu Arg Ala Leu Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala
50 55 60

Gln Thr Glu Thr Glu Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu
65 70 75 80

Leu Leu Glu Ala Val Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala
85 90 95

Arg Ala Gly Phe Glu Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly
100 105 110

Pro Lys Glu Ser Arg Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro
115 120 125

Gln Ala Ala Gly Val Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys
130 135 140

Ala Glu Ile Val Ser Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala
145 150 155 160

Glu Ala Lys Ala Gln Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val
165 170 175

Met Val Asp Gly Asp Val Val Glu Phe Arg Phe Asn Val
180 185

<210> 217

<211> 1626

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1603)

<223> RXA02376

<400> 217

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tcggcgcccg ttttatcccg atcaggagtg acaccgtttt atg aac cga ttt att 115

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gtc Val	tcg Ser	gtg Val	cac His 25	cgc Arg	gaa Glu	aaa Lys	ttc Phe	aag Lys 30	cca Pro	ctt Leu	ggt Gly	gga Gly	cca Pro 35	gac Asp	ggc Gly	211
ggc Gly	aac Asn	ggc Gly 40	ggc Gly	cac His	ggt Gly	gga Gly	gac Asp 45	atc Ile	atc Ile	ttg Leu	gaa Glu	gtc Val 50	acc Thr	gca Ala	cag Gln	259
gtc Val	cac His 55	acc Thr	ctg Leu	ctt Leu	gac Asp	ttc Phe 60	cac His	ttc Phe	cac His	cca Pro	cac His 65	gtg Val	aag Lys	gcc Ala	gag Glu	307
cgc Arg 70	ggc Gly	gct Ala	aac Asn	ggc Gly	gct Ala 75	ggc Gly	gat Asp	cat His	cgc Arg	aac Asn 80	ggt Gly	gcc Ala	cga Arg	ggc Gly	aag Lys 85	355
gac Asp	ctt Leu	gtc Val	ttg Leu	gaa Glu 90	gtt Val	cca Pro	cca Pro	gga Gly	act Thr 95	gtc Val	gtg Val	ctt Leu	aat Asn	gaa Glu 100	aag Lys	403
ggc Gly	gag Glu	act Thr	ctg Leu 105	gca Ala	gac Asp	ctg Leu	acc Thr	agc Ser 110	gtg Val	ggc Gly	atg Met	aag Lys 115	ttc Phe	atc Ile	gct Ala	451
gct Ala	gct Ala	ggc Gly 120	ggc Gly	aac Asn	ggc Gly	ggt Gly	ttg Leu 125	ggt Gly	aac Asn	gca Ala	gcg Ala	ctt Leu 130	gcc Ala	tcc Ser	aag Lys	499
gct Ala	cgt Arg 135	aag Lys	gcc Ala	cca Pro	ggc Gly	ttc Phe 140	gcc Ala	ctg Leu	atc Ile	ggt Gly	gag Glu 145	cca Pro	ggc Gly	gag Glu	gcc Ala	547
cac His 150	gac Asp	ttg Leu	att Ile	ctt Leu	gaa Glu 155	ctc Leu	aaa Lys	tcc Ser	atg Met	gca Ala 160	gat Asp	gtg Val	gga Gly	ttg Leu	gtg Val 165	595
ggc Gly	ttc Phe	cca Pro	tca Ser	gcc Ala 170	ggc Gly	aaa Lys	tca Ser	tca Ser	ctg Leu 175	att Ile	tct Ser	gtg Val	atg Met	tct Ser 180	gca Ala	643
gca Ala	aag Lys	cca Pro	aag Lys 185	atc Ile	ggt Gly	gat Asp	tac Tyr	cca Pro 190	ttc Phe	acc Thr	acc Thr	ctg Leu	cag Gln 195	cca Pro	aac Asn	691
ctc Leu	ggc Gly	gta Val 200	gtt Val	aac Asn	gtt Val	ggt Gly	cat His 205	gag Glu	act Thr	ttc Phe	acc Thr 210	atg Met	gca Ala	gac Asp	gtg Val	739
cct Pro	ggt Gly 215	ttg Leu	atc Ile	cct Pro	ggt Gly	gct Ala 220	tct Ser	gag Glu	ggc Gly	aag Lys	ggc Gly 225	ttg Leu	ggt Gly	ctg Leu	gat Asp	787
ttc Phe	ttg Leu	cgc Arg	cac His	att Ile	gag Glu	cgc Arg	acc Thr	tcc Ser	gtg Val	ctg Leu	gtt Val	cac His	ggt Val	gtc Val	gat Asp	835

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acc gca acg atg gat cca ggc cgc gat ccg atc tct gat att gag gct	883			
Thr Ala Thr Met Asp Pro Gly Arg Asp Pro Ile Ser Asp Ile Glu Ala				
250 255 260				
ttg gaa gca gaa ctt gcc gcc tac cag tcg gct ttg gat gaa gac acc	931			
Leu Glu Ala Glu Leu Ala Ala Tyr Gln Ser Ala Leu Asp Glu Asp Thr				
265 270 275				
gga ctt ggt gac ttg agc cag cgc cct cgc ctt gtt gtg ttg aac aag	979			
Gly Leu Gly Asp Leu Ser Gln Arg Pro Arg Leu Val Val Leu Asn Lys				
280 285 290				
gct gat gtc cct gag gct gaa gag ctt gct gag ttc ctc aaa gaa gat	1027			
Ala Asp Val Pro Glu Ala Glu Glu Leu Ala Glu Phe Leu Lys Glu Asp				
295 300 305				
att gag aag caa ttc gga tgg ccc gtg ttc att atc tcc gca gtg gca	1075			
Ile Glu Lys Gln Phe Gly Trp Pro Val Phe Ile Ile Ser Ala Val Ala				
310 315 320 325				
cgc aag ggc ttg gat cct ttg aag tac aag ctg ctg gaa atc gtc cag	1123			
Arg Lys Gly Leu Asp Pro Leu Lys Tyr Lys Leu Leu Glu Ile Val Gln				
330 335 340				
gat gcc cga aag aag cgt cca aag gag aag gct gag tct gtc atc att	1171			
Asp Ala Arg Lys Lys Arg Pro Lys Glu Lys Ala Glu Ser Val Ile Ile				
345 350 355				
aag cct aag gct gtt gat cac cgc act aag ggg cag ttc cag atc aag	1219			
Lys Pro Lys Ala Val Asp His Arg Thr Lys Gly Gln Phe Gln Ile Lys				
360 365 370				
cct gac cca gag gtt cag ggc gga ttc atc atc acc ggc gaa aag cca	1267			
Pro Asp Pro Glu Val Gln Gly Gly Phe Ile Ile Thr Gly Glu Lys Pro				
375 380 385				
gag cgc tgg att ttg cag acc gac ttt gaa aac gac gaa gca gtt ggc	1315			
Glu Arg Trp Ile Leu Gln Thr Asp Phe Glu Asn Asp Glu Ala Val Gly				
390 395 400 405				
tac ctg gct gac cgt ctg gcc aag ttg ggc att gag gac ggg ctt cgt	1363			
Tyr Leu Ala Asp Arg Leu Ala Lys Leu Gly Ile Glu Asp Gly Leu Arg				
410 415 420				
aag gca gga gca cat gtg ggt gca aac gtc acc atc gga ggc att tcc	1411			
Lys Ala Gly Ala His Val Gly Ala Asn Val Thr Ile Gly Gly Ile Ser				
425 430 435				
ttc gag tgg gag cca atg acc acc gct ggc gac gat cca gtc ctt acc	1459			
Phe Glu Trp Glu Pro Met Thr Thr Ala Gly Asp Asp Pro Val Leu Thr				
440 445 450				
gga cgt ggc acc gat gtg cgc ctt gaa cag acc tct cgt atc tct gct	1507			
Gly Arg Gly Thr Asp Val Arg Leu Glu Gln Thr Ser Arg Ile Ser Ala				
455 460 465				
gca gag cgt aaa cgc gca tct cag gta cgt cgt ggc ctc atc gat gag	1555			
Ala Glu Arg Lys Arg Ala Ala Ser Gln Val Arg Arg Gly Leu Ile Asp Glu				
470 475 480 485				

ttg gat tat ggc gag gac caa gag gct tcc cgc gaa cgc tgg gaa gga 1603
 Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg Glu Arg Trp Glu Gly
 490 495 500

taaaaccgag cacttttcag gtc 1626

<210> 218

<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Asn Arg Phe Ile Asp Arg Val Val Leu His Leu Ala Ala Gly Asp
 1 5 10 15

Gly Gly Asn Gly Cys Val Ser Val His Arg Glu Lys Phe Lys Pro Leu
 20 25 30

Gly Gly Pro Asp Gly Gly Asn Gly Gly His Gly Gly Asp Ile Ile Leu
 35 40 45

Glu Val Thr Ala Gln Val His Thr Leu Leu Asp Phe His Phe His Pro
 50 55 60

His Val Lys Ala Glu Arg Gly Ala Asn Gly Ala Gly Asp His Arg Asn
 65 70 75 80

Gly Ala Arg Gly Lys Asp Leu Val Leu Glu Val Pro Pro Gly Thr Val
 85 90 95

Val Leu Asn Glu Lys Gly Glu Thr Leu Ala Asp Leu Thr Ser Val Gly
 100 105 110

Met Lys Phe Ile Ala Ala Ala Gly Gly Asn Gly Gly Leu Gly Asn Ala
 115 120 125

Ala Leu Ala Ser Lys Ala Arg Lys Ala Pro Gly Phe Ala Leu Ile Gly
 130 135 140

Glu Pro Gly Glu Ala His Asp Leu Ile Leu Glu Leu Lys Ser Met Ala
 145 150 155 160

Asp Val Gly Leu Val Gly Phe Pro Ser Ala Gly Lys Ser Ser Leu Ile
 165 170 175

Ser Val Met Ser Ala Ala Lys Pro Lys Ile Gly Asp Tyr Pro Phe Thr
 180 185 190

Thr Leu Gln Pro Asn Leu Gly Val Val Asn Val Gly His Glu Thr Phe
 195 200 205

Thr Met Ala Asp Val Pro Gly Leu Ile Pro Gly Ala Ser Glu Gly Lys
 210 215 220

Gly Leu Gly Leu Asp Phe Leu Arg His Ile Glu Arg Thr Ser Val Leu
 225 230 235 240

Val His Val Val Asp Thr Ala Thr Met Asp Pro Gly Arg Asp Pro Ile
 245 250 255

Ser Asp Ile Glu Ala Leu Glu Ala Glu Leu Ala Ala Tyr Gln Ser Ala
260 265 270

Leu Asp Glu Asp Thr Gly Leu Gly Asp Leu Ser Gln Arg Pro Arg Leu
275 280 285

Val Val Leu Asn Lys Ala Asp Val Pro Glu Ala Glu Glu Leu Ala Glu
290 295 300

Phe Leu Lys Glu Asp Ile Glu Lys Gln Phe Gly Trp Pro Val Phe Ile
305 310 315 320

Ile Ser Ala Val Ala Arg Lys Gly Leu Asp Pro Leu Lys Tyr Lys Leu
325 330 335

Leu Glu Ile Val Gln Asp Ala Arg Lys Lys Arg Pro Lys Glu Lys Ala
340 345 350

Glu Ser Val Ile Ile Lys Pro Lys Ala Val Asp His Arg Thr Lys Gly
355 360 365

Gln Phe Gln Ile Lys Pro Asp Pro Glu Val Gln Gly Gly Phe Ile Ile
370 375 380

Thr Gly Glu Lys Pro Glu Arg Trp Ile Leu Gln Thr Asp Phe Glu Asn
385 390 395 400

Asp Glu Ala Val Gly Tyr Leu Ala Asp Arg Leu Ala Lys Leu Gly Ile
405 410 415

Glu Asp Gly Leu Arg Lys Ala Gly Ala His Val Gly Ala Asn Val Thr
420 425 430

Ile Gly Gly Ile Ser Phe Glu Trp Glu Pro Met Thr Thr Ala Gly Asp
435 440 445

Asp Pro Val Leu Thr Gly Arg Gly Thr Asp Val Arg Leu Glu Gln Thr
450 455 460

Ser Arg Ile Ser Ala Ala Glu Arg Lys Arg Ala Ser Gln Val Arg Arg
465 470 475 480

Gly Leu Ile Asp Glu Leu Asp Tyr Gly Glu Asp Gln Glu Ala Ser Arg
485 490 495

Glu Arg Trp Glu Gly
500

<210> 219

<211> 605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(582)

<223> RXA01065

<400> 219

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Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly
  1          5          10          15

atc atc acc aaa gca gac agc gtc tca cgt gac ttg gtt gcg gcc caa 96
Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln
          20          25          30

ctg atg gct gtc cat gag ctg ctc ggc gga aac agc gag gta gtc cca 144
Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro
          35          40          45

gtg tct tcc acc tcg ggg gaa aac gtc gaa acg ctt att aag gtc atg 192
Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met
          50          55          60

acc gac ctg ctg cct gaa ggc ccc aag ttc tac ccg gat gat cac atc 240
Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
          65          70          75          80

acc gat gag gac acc aac acc cgc atc gcg gaa gcc atc cgc gaa gca 288
Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
          85          90          95

gca ctg tct ggc ttg aag aac gaa ctg ccg cac tcc gtc gca gtt gag 336
Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu
          100          105          110

gtt gat gaa atc ctg cca gac cca gaa cgc aac ggt gtc ctg gct gtg 384
Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val
          115          120          125

cac gcc atc atc tac gtc gag cgt gtt ggt cag aaa gac atc atc gtc 432
His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val
          130          135          140

gga cac aag gga cag cgc ctg ggg cgc atc atc cac acc tca cgc caa 480
Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln
          145          150          155          160

gac atc atc aag atc ctc ggc caa aac gta ttc ctt gac ctg cgc atc 528
Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
          165          170          175

aag gtg ctg aag aac tgg caa tcc gat cca aag gct ttg aac cgc ctg 576
Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
          180          185          190

ggc ttc tagctttaag ggggtgagtt cat 605
Gly Phe

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<210> 220

<211> 194

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly
  1          5          10          15

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Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Ala Gln
 20 25 30
 Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro
 35 40 45
 Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met
 50 55 60
 Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
 65 70 75 80
 Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
 85 90 95
 Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu
 100 105 110
 Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val
 115 120 125
 His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val
 130 135 140
 Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln
 145 150 155 160
 Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
 165 170 175
 Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
 180 185 190

Gly Phe

<210> 221
 <211> 1650
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1627)
 <223> RXA02232

<400> 221
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 ctagccttgg cgacagcaga cgtgaaacaa tagataaaca atg gat gaa aag aaa 115
 Met Asp Glu Lys Lys
 1 5

 aac tta agt cat gat gaa ctt ctc gct cag gcc ttc cgc ggt cac aaa 163
 Asn Leu Ser His Asp Glu Leu Leu Ala Gln Ala Phe Arg Gly His Lys
 10 15 20

 aat acc gtg cgc cca gga tct gac gag acc tca ggt ttt gat ctc agt 211
 Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser Gly Phe Asp Leu Ser

25										30					35					
ggt	ttt	atc	cga	gct	gaa	gaa	cca	tca	act	ggt	gat	ctc	gac	cta	gag	259				
Gly	Phe	Ile	Arg	Ala	Glu	Glu	Pro	Ser	Thr	Gly	Asp	Leu	Asp	Leu	Glu					
		40					45					50								
gcc	cgc	gat	gcc	caa	cgt	cgc	cgg	gac	acc	gaa	atc	cac	gct	gat	gaa	307				
Ala	Arg	Asp	Ala	Gln	Arg	Arg	Arg	Asp	Thr	Glu	Ile	His	Ala	Asp	Glu					
	55					60					65									
gca	gca	gat	ggc	tac	gag	gtt	gag	tac	cga	aag	ctg	cga	ctt	gag	cgc	355				
Ala	Ala	Asp	Gly	Tyr	Glu	Val	Glu	Tyr	Arg	Lys	Leu	Arg	Leu	Glu	Arg					
70					75					80					85					
gtt	atc	tta	gtg	ggc	gtg	tgg	acc	gaa	ggt	acc	acc	gca	gaa	att	gac	403				
Val	Ile	Leu	Val	Gly	Val	Trp	Thr	Glu	Gly	Thr	Thr	Ala	Glu	Ile	Asp					
				90					95					100						
gcc	agc	ctt	gcg	gaa	ctt	gca	gcg	ttg	gct	gat	acc	gcc	ggc	gct	gag	451				
Ala	Ser	Leu	Ala	Glu	Leu	Ala	Ala	Leu	Ala	Asp	Thr	Ala	Gly	Ala	Glu					
			105					110					115							
gtt	att	gaa	acg	ctg	tac	caa	aag	cgc	gat	aaa	cca	gat	cct	gga	acc	499				
Val	Ile	Glu	Thr	Leu	Tyr	Gln	Lys	Arg	Asp	Lys	Pro	Asp	Pro	Gly	Thr					
		120					125					130								
tac	att	ggt	tcc	ggc	aag	gtt	cgg	gag	tta	aag	gag	atc	atc	gaa	gcc	547				
Tyr	Ile	Gly	Ser	Gly	Lys	Val	Arg	Glu	Leu	Lys	Glu	Ile	Ile	Glu	Ala					
		135				140					145									
act	agt	gca	gat	acc	gtg	gtg	tgc	gat	ggt	gaa	ctt	agc	cct	tcc	cag	595				
Thr	Ser	Ala	Asp	Thr	Val	Val	Cys	Asp	Gly	Glu	Leu	Ser	Pro	Ser	Gln					
150					155				160						165					
ctc	gtg	gca	tta	gag	cgc	gaa	ctt	gat	atc	aag	gtc	att	gac	cgc	acc	643				
Leu	Val	Ala	Leu	Glu	Arg	Glu	Leu	Asp	Ile	Lys	Val	Ile	Asp	Arg	Thr					
				170					175					180						
atg	ctg	att	ctg	gat	atc	ttc	gcc	cag	cac	gct	aaa	tcg	cgc	gaa	ggt	691				
Met	Leu	Ile	Leu	Asp	Ile	Phe	Ala	Gln	His	Ala	Lys	Ser	Arg	Glu	Gly					
			185					190					195							
aaa	gcc	caa	gtc	gcg	ttg	gcg	cag	atg	gaa	tac	ctg	att	agc	cgt	gtg	739				
Lys	Ala	Gln	Val	Ala	Leu	Ala	Gln	Met	Glu	Tyr	Leu	Ile	Ser	Arg	Val					
		200					205					210								
cgt	ggt	tgg	ggt	gga	aac	ctc	tcc	agg	cag	gcc	ggt	ggt	cgt	gca	ggt	787				
Arg	Gly	Trp	Gly	Gly	Asn	Leu	Ser	Arg	Gln	Ala	Gly	Gly	Arg	Ala	Gly					
	215					220					225									
tct	aat	ggt	ggt	gtg	ggt	ctg	cgt	ggt	cca	ggt	gaa	acc	aaa	att	gaa	835				
Ser	Asn	Gly	Gly	Val	Gly	Leu	Arg	Gly	Pro	Gly	Glu	Thr	Lys	Ile	Glu					
230					235					240					245					
gca	gac	cgc	cgt	cgt	ctt	cga	tcg	gat	atg	gct	cgc	ctg	cgc	agg	gaa	883				
Ala	Asp	Arg	Arg	Arg	Leu	Arg	Ser	Asp	Met	Ala	Arg	Leu	Arg	Arg	Glu					
				250					255					260						
ctt	tcg	ggg	ctg	gat	acg	tcg	aga	agc	att	aaa	aga	gcg	caa	cgc	gca	931				
Leu	Ser	Gly	Leu	Asp	Thr	Ser	Arg	Ser	Ile	Lys	Arg	Ala	Gln	Arg	Ala					
			265					270					275							

gcc tcc ctg gtg ccg cag atc gcc atc gct ggc tac acg aac gcc ggc	979
Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly Tyr Thr Asn Ala Gly	
280 285 290	
aaa tct tcg ctg att aac gcg atg acc ggc gcg ggt gtg ctg gtg gag	1027
Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala Gly Val Leu Val Glu	
295 300 305	
aac gcg ctg ttc gcc acg ctt gat cca aca acc aga aaa gcc gag ctt	1075
Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr Arg Lys Ala Glu Leu	
310 315 320 325	
gcc gac ggc cga cac gtc gtg ttc acg gac acc gtc ggc ttt gtg cga	1123
Ala Asp Gly Arg His Val Val Phe Thr Asp Thr Val Gly Phe Val Arg	
330 335 340	
cac ctg ccg acc tct ctg gtt gag gcg ttc aaa tct acg ctg gaa gaa	1171
His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys Ser Thr Leu Glu Glu	
345 350 355	
gtc gtg gag gcg gac ctc atg ctg cac gtg gtg gat gga tcc gat ccg	1219
Val Val Glu Ala Asp Leu Met Leu His Val Val Asp Gly Ser Asp Pro	
360 365 370	
ttc ccg ctg aag cag atc gac gct gtg aac acc gtg att agc gat att	1267
Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr Val Ile Ser Asp Ile	
375 380 385	
gtg cga tcc acc ggt gcg gtg cca cca cca gag atc atc gtg gtg aac	1315
Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu Ile Ile Val Val Asn	
390 395 400 405	
aaa att gac caa gct gat ccg ctg acg ctg gca gaa cta cgc cac gcc	1363
Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala Glu Leu Arg His Ala	
410 415 420	
gtc gac gat gtg gtg ttt gtc tct gcg ctg aca ggg gag gga att aag	1411
Val Asp Asp Val Val Phe Val Ser Ala Leu Thr Gly Glu Gly Ile Lys	
425 430 435	
gag ctg gaa gct cgc atc gaa cta ttc ctc aac tcc agg gag gcg cac	1459
Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn Ser Arg Asp Ala His	
440 445 450	
cta ctg ctg aaa atc ccg ttc acc cgt ggc gat att gtg tcc cgc ctg	1507
Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp Ile Val Ser Arg Leu	
455 460 465	
cac cag cat ggc acc gtt ctc agc gaa gac tac gcc gaa gac ggc acc	1555
His Gln His Gly Thr Val Leu Ser Glu Asp Tyr Ala Glu Asp Gly Thr	
470 475 480 485	
ttg atg gat gtg cgt atc ccc acc caa ttg gcc caa gag ctg cag agt	1603
Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala Gln Glu Leu Gln Ser	
490 495 500	
tac gtt gta gaa ccc acc tct gcc taactgtcga tttcccaaga gcc	1650
Tyr Val Val Glu Pro Thr Ser Ala	
505	

<400> 222															
Met 1	Asp	Glu	Lys	Lys 5	Asn	Leu	Ser	His	Asp 10	Glu	Leu	Leu	Ala	Gln 15	Ala
Phe	Arg	Gly	His 20	Lys	Asn	Thr	Val	Arg 25	Pro	Gly	Ser	Asp	Glu 30	Thr	Ser
Gly	Phe	Asp 35	Leu	Ser	Gly	Phe	Ile 40	Arg	Ala	Glu	Glu	Pro 45	Ser	Thr	Gly
Asp	Leu 50	Asp	Leu	Glu	Ala	Arg 55	Asp	Ala	Gln	Arg	Arg 60	Arg	Asp	Thr	Glu
Ile 65	His	Ala	Asp	Glu	Ala 70	Ala	Asp	Gly	Tyr	Glu 75	Val	Glu	Tyr	Arg	Lys 80
Leu	Arg	Leu	Glu	Arg 85	Val	Ile	Leu	Val	Gly 90	Val	Trp	Thr	Glu	Gly 95	Thr
Thr	Ala	Glu	Ile 100	Asp	Ala	Ser	Leu	Ala 105	Glu	Leu	Ala	Ala	Leu 110	Ala	Asp
Thr	Ala	Gly 115	Ala	Glu	Val	Ile	Glu 120	Thr	Leu	Tyr	Gln	Lys 125	Arg	Asp	Lys
Pro	Asp 130	Pro	Gly	Thr	Tyr	Ile 135	Gly	Ser	Gly	Lys	Val 140	Arg	Glu	Leu	Lys
Glu 145	Ile	Ile	Glu	Ala	Thr 150	Ser	Ala	Asp	Thr	Val 155	Val	Cys	Asp	Gly	Glu 160
Leu	Ser	Pro	Ser	Gln 165	Leu	Val	Ala	Leu	Glu 170	Arg	Glu	Leu	Asp	Ile 175	Lys
Val	Ile	Asp	Arg 180	Thr	Met	Leu	Ile 185	Leu	Asp	Ile	Phe	Ala	Gln 190	His	Ala
Lys	Ser	Arg 195	Glu	Gly	Lys	Ala	Gln 200	Val	Ala	Leu	Ala	Gln 205	Met	Glu	Tyr
Leu 210	Ile	Ser	Arg	Val	Arg	Gly 215	Trp	Gly	Gly	Asn	Leu 220	Ser	Arg	Gln	Ala
Gly 225	Gly	Arg	Ala	Gly	Ser 230	Asn	Gly	Gly	Val	Gly 235	Leu	Arg	Gly	Pro	Gly 240
Glu	Thr	Lys	Ile	Glu 245	Ala	Asp	Arg	Arg	Arg 250	Leu	Arg	Ser	Asp	Met 255	Ala
Arg	Leu	Arg	Arg 260	Glu	Leu	Ser	Gly	Leu 265	Asp	Thr	Ser	Arg	Ser 270	Ile	Lys
Arg	Ala	Gln 275	Arg	Ala	Ala	Ser	Leu 280	Val	Pro	Gln	Ile	Ala 285	Ile	Ala	Gly

Tyr Thr Asn Ala Gly Lys Ser Ser Leu Ile Asn Ala Met Thr Gly Ala
 290 295 300
 Gly Val Leu Val Glu Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr
 305 310 315 320
 Arg Lys Ala Glu Leu Ala Asp Gly Arg His Val Val Phe Thr Asp Thr
 325 330 335
 Val Gly Phe Val Arg His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys
 340 345 350
 Ser Thr Leu Glu Glu Val Val Glu Ala Asp Leu Met Leu His Val Val
 355 360 365
 Asp Gly Ser Asp Pro Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr
 370 375 380
 Val Ile Ser Asp Ile Val Arg Ser Thr Gly Ala Val Pro Pro Pro Glu
 385 390 395 400
 Ile Ile Val Val Asn Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala
 405 410 415
 Glu Leu Arg His Ala Val Asp Asp Val Val Phe Val Ser Ala Leu Thr
 420 425 430
 Gly Glu Gly Ile Lys Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn
 435 440 445
 Ser Arg Asp Ala His Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp
 450 455 460
 Ile Val Ser Arg Leu His Gln His Gly Thr Val Leu Ser Glu Asp Tyr
 465 470 475 480
 Ala Glu Asp Gly Thr Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala
 485 490 495
 Gln Glu Leu Gln Ser Tyr Val Val Glu Pro Thr Ser Ala
 500 505

<210> 223

<211> 194

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(171)

<223> RXA00848

<400> 223

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Thr	Thr	Val	Thr	Leu	Ala	Lys	Ala	Arg	Ser	Leu	Ser	Leu	Asp	Glu	Ala	
1				5				10						15		
ctg	gag	ttc	tgt	ggc	gtc	gac	gag	tgc	gtc	gag	gtt	acc	cct	gat	gtt	96
Leu	Glu	Phe	Cys	Gly	Val	Asp	Glu	Cys	Val	Glu	Val	Thr	Pro	Asp	Val	
			20					25						30		

```

ctg cgc atc cgc aag gtc atc ctg aac gct act gag cgt ggc cgt gca 144
Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala
      35              40              45

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```

cgt tcc cgt gcg aag agc ctg aac aag taattctctt ttagttaaga gtt 194
Arg Ser Arg Ala Lys Ser Leu Asn Lys
      50              55

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<210> 224

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

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Thr Thr Val Thr Leu Ala Lys Ala Arg Ser Leu Ser Leu Asp Glu Ala
  1              5              10              15

```

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Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val
      20              25              30

```

```

Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala
      35              40              45

```

```

Arg Ser Arg Ala Lys Ser Leu Asn Lys
      50              55

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<210> 225

<211> 469

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> FRXA00839

<400> 225

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cacaatgtgc ggaacgggcg ataatgcgag tacagtgata ccgttctaaa acaatggact 60

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cgttttacaa gtcctccata cttctttatc cggcaggaga atg ccc cca gtg acc 115
                                     Met Pro Pro Val Thr
                                     1              5

```

```

cac cca gag ttt cgt aac gta gcg att gtc gcg cac gtt gac cac gga 163
His Pro Glu Phe Arg Asn Val Ala Ile Val Ala His Val Asp His Gly
      10              15              20

```

```

aag acc aca ctc gtt aat gcc atg ctt gaa cag tct ggc gta ttc agt 211
Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln Ser Gly Val Phe Ser
      25              30              35

```

```

gac cac ggt gaa gta gcc gac cgt gtg atg gac tcc ggt gac ctg gaa 259
Asp His Gly Glu Val Ala Asp Arg Val Met Asp Ser Gly Asp Leu Glu
      40              45              50

```

```

aag gaa aag ggc atc acc atc ctt gcc aag aac acc gcg att cgt cgt 307
Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile Arg Arg
      55              60              65

```



```

aaa ggc gct ggc aag gac ggc aat gac ctg att atc aac gtc att gac 355
Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile Ile Asn Val Ile Asp
 70                      75                      80                      85

acc cca ggc cac gct gac ttc ggt ggc gaa gtt gag cgc gca ctg tcc 403
Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val Glu Arg Ala Leu Ser
                      90                      95                      100

atg gtt gac ggc gtt gtc ctt ctg gtt gac gca tct gaa ggc cca ctg 451
Met Val Asp Gly Val Val Leu Leu Val Asp Ala Ser Glu Gly Pro Leu
                      105                      110                      115

cct cag acc cga ttc gtg
Pro Gln Thr Arg Phe Val
                      120

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<210> 226
<211> 123
<212> PRT
<213> Corynebacterium glutamicum

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<400> 226
Met Pro Pro Val Thr His Pro Glu Phe Arg Asn Val Ala Ile Val Ala
 1                      5                      10                      15

His Val Asp His Gly Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln
                20                      25                      30

Ser Gly Val Phe Ser Asp His Gly Glu Val Ala Asp Arg Val Met Asp
                35                      40                      45

Ser Gly Asp Leu Glu Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn
 50                      55                      60

Thr Ala Ile Arg Arg Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile
 65                      70                      75                      80

Ile Asn Val Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val
                85                      90                      95

Glu Arg Ala Leu Ser Met Val Asp Gly Val Val Leu Leu Val Asp Ala
                100                      105                      110

Ser Glu Gly Pro Leu Pro Gln Thr Arg Phe Val
 115                      120

```

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<210> 227
<211> 903
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(903)
<223> FRXA00845

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<400> 227
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ttg	cgt	aag	ggc	cag	cag	gtt	gca	tgg	att	cac	tac	gat	gaa	gaa	ggg	96	
Leu	Arg	Lys	Gly 20	Gln	Gln	Val	Ala	Trp 25	Ile	His	Tyr	Asp	Glu 30	Glu	Gly		
aac	cag	cac	acc	aag	acc	gct	aag	atc	gca	gag	ctt	ctg	gct	acc	gtt	144	
Asn	Gln	His 35	Thr	Lys	Thr	Ala	Lys 40	Ile	Ala	Glu	Leu	Leu 45	Ala	Thr	Val		
ggc	gtt	gcc	cgc	gtt	cct	gct	acc	gaa	gtt	gtt	gca	ggg	gac	atc	gct	192	
Gly	Val 50	Ala	Arg	Val	Pro	Ala 55	Thr	Glu	Val	Val	Ala 60	Gly	Asp	Ile	Ala		
gct	atc	tcc	ggc	atc	gaa	gac	atc	atg	att	ggc	gat	acc	ctc	gcg	gat	240	
Ala	Ile 65	Ser	Gly	Ile	Glu 70	Asp	Ile	Met	Ile	Gly 75	Asp	Thr	Leu	Ala	Asp 80		
cct	gag	aac	cca	gtt	gca	ctg	cct	cgc	atc	acc	gtt	gat	gag	cca	gca	288	
Pro	Glu	Asn	Pro	Val 85	Ala	Leu	Pro	Arg	Ile 90	Thr	Val	Asp	Glu	Pro 95	Ala		
ctg	tcc	atg	acc	atc	ggg	gtg	aac	acc	tca	cca	atg	gct	ggg	cgt	ggc	336	
Leu	Ser	Met 100	Thr	Ile	Gly	Val	Asn 105	Thr	Ser	Pro	Met	Ala	Gly 110	Arg	Gly		
ggc	gga	gac	aag	ctg	acc	gca	cgt	gtg	gtc	aag	gct	cgt	ctt	gag	aac	384	
Gly	Gly	Asp 115	Lys	Leu	Thr	Ala	Arg 120	Val	Val	Lys	Ala	Arg 125	Leu	Glu	Asn		
gaa	ctg	atc	ggg	aac	gtg	tcc	ctg	aag	gtc	aac	cca	act	gag	cgc	cca	432	
Glu	Leu 130	Ile	Gly	Asn	Val	Ser 135	Leu	Lys	Val	Asn 140	Pro	Thr	Glu	Arg	Pro		
gat	acc	tgg	gaa	gtt	cag	ggg	cgt	ggc	gaa	atg	gct	ctg	tcc	atc	ctc	480	
Asp	Thr	Trp	Glu	Val	Gln 150	Gly	Arg	Gly	Glu	Met 155	Ala	Leu	Ser	Ile	Leu 160		
gtt	gag	acc	atg	cgt	cgc	gaa	ggc	ttc	gag	ctc	acc	gtt	ggg	aag	cca	528	
Val	Glu	Thr	Met 165	Arg	Arg	Glu	Gly	Phe 170	Glu	Leu	Thr	Val	Gly 175	Lys	Pro		
cag	gtt	gtt	acc	cag	acc	atc	gac	ggc	aag	ctg	cac	gag	cct	tac	gag	576	
Gln	Val	Val	Thr 180	Gln	Thr	Ile	Asp	Gly 185	Lys	Leu	His	Glu	Pro 190	Tyr	Glu		
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Ile	Ile	Val 195	Ile	Asp	Val	Pro	Ser 200	Glu	Tyr	Gln	Gly	Asn 205	Val	Thr	Gln		
ctg	ctg	gct	acc	cgc	aag	ggc	ctc	atg	cag	tcc	atg	tcc	acc	acc	cca	672	
Leu	Leu	Ala 210	Thr	Arg	Lys	Gly 215	Leu	Met	Gln	Ser	Met 220	Ser	Thr	Thr	Pro		
ggg	tcc	gac	tgg	atc	cgc	atg	gaa	ttc	cgt	att	cct	gct	cgt	ggc	ctg	720	
Gly	Ser	Asp	Trp	Ile	Arg 230	Met	Glu	Phe	Arg	Ile 235	Pro	Ala	Arg	Gly	Leu 240		
att	ggg	ttc	cgt	acc	cag	ttc	atg	act	gaa	acc	cgt	ggg	acc	ggg	atc	768	
Ile	Gly	Phe	Arg	Thr	Gln	Phe	Met	Thr	Glu	Thr	Arg	Gly	Thr	Gly	Ile		

245										250					255					
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Ala	Asn	Ser	Tyr	Ser	Asp	Gly	Met	Asp	Val	Trp	Ala	Gly	Glu	Ile	Lys					
			260					265					270							
ggc	cgc	gca	cac	ggc	tcc	ttg	gtt	gct	gac	cgt	tcc	ggc	cag	atc	acc	864				
Gly	Arg	Ala	His	Gly	Ser	Leu	Val	Ala	Asp	Arg	Ser	Gly	Gln	Ile	Thr					
		275					280					285								
gct	tac	gct	ctg	acc	cag	ctg	gca	gac	cgt	ggc	agc	ttc				903				
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<213> Corynebacterium glutamicum

<400> 228

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Asn	Gln	His	Thr	Lys	Thr	Ala	Lys	Ile	Ala	Glu	Leu	Leu	Ala	Thr	Val
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Gly	Val	Ala	Arg	Val	Pro	Ala	Thr	Glu	Val	Val	Ala	Gly	Asp	Ile	Ala
	50					55					60				
Ala	Ile	Ser	Gly	Ile	Glu	Asp	Ile	Met	Ile	Gly	Asp	Thr	Leu	Ala	Asp
65					70					75					80
Pro	Glu	Asn	Pro	Val	Ala	Leu	Pro	Arg	Ile	Thr	Val	Asp	Glu	Pro	Ala
				85				90						95	
Leu	Ser	Met	Thr	Ile	Gly	Val	Asn	Thr	Ser	Pro	Met	Ala	Gly	Arg	Gly
			100					105					110		
Gly	Gly	Asp	Lys	Leu	Thr	Ala	Arg	Val	Val	Lys	Ala	Arg	Leu	Glu	Asn
		115					120					125			
Glu	Leu	Ile	Gly	Asn	Val	Ser	Leu	Lys	Val	Asn	Pro	Thr	Glu	Arg	Pro
	130					135					140				
Asp	Thr	Trp	Glu	Val	Gln	Gly	Arg	Gly	Glu	Met	Ala	Leu	Ser	Ile	Leu
145					150					155					160
Val	Glu	Thr	Met	Arg	Arg	Glu	Gly	Phe	Glu	Leu	Thr	Val	Gly	Lys	Pro
				165					170					175	
Gln	Val	Val	Thr	Gln	Thr	Ile	Asp	Gly	Lys	Leu	His	Glu	Pro	Tyr	Glu
			180					185					190		
Ile	Ile	Val	Ile	Asp	Val	Pro	Ser	Glu	Tyr	Gln	Gly	Asn	Val	Thr	Gln
		195				200						205			
Leu	Leu	Ala	Thr	Arg	Lys	Gly	Leu	Met	Gln	Ser	Met	Ser	Thr	Thr	Pro

210	215	220
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Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile 245 250 255		
Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys 260 265 270		
Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr 275 280 285		
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<211> 581

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<223> RXA02365

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ggt ggc atg gac tac ctt tgc gag gac cgc gtg gag ctg cgc tac acc Gly Gly Met Asp Tyr Leu Ser Glu Asp Arg Val Glu Leu Arg Tyr Thr 15 20 25	99
atg cct ttg ggt gag atc atc ttt gac ttc ttc gat atg ttg aag tct Met Pro Leu Gly Glu Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser 30 35 40	147
cgc acc aag ggt tac gct tgc ctg aac tac gag gaa gct ggc gag cag Arg Thr Lys Gly Tyr Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln 45 50 55	195
act gcc gac ctg gtc aag gta gat atc ttg ctc caa ggt gaa cct gtg Thr Ala Asp Leu Val Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val 60 65 70 75	243
gat gca ttc tct gcg atc gtg cac cgc gat aat gcg cag tgg tac gga Asp Ala Phe Ser Ala Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly 80 85 90	291
aac aag atg act gtg aag ctg aag gaa ctg atc cct cgc cag cag ttc Asn Lys Met Thr Val Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe 95 100 105	339
gaa gtt cct gtg cag gca gcc att ggt tcc aag gtt atc gct cgt gaa Glu Val Pro Val Gln Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu 110 115 120	387

aac att cgt gca ctg cgc aag gac gtg ttg gcg aag tgt tac ggt ggc 435
 Asn Ile Arg Ala Leu Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly
 125 130 135

gat att tcc cgt aag cgc aag ctt ctg gaa aag cag aag gct ggt aag 483
 Asp Ile Ser Arg Lys Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys
 140 145 150 155

aag cgc atg aag aac atc ggt tgc gtc gag gtt cct cag gaa gca ttc 531
 Lys Arg Met Lys Asn Ile Gly Ser Val Glu Val Pro Gln Glu Ala Phe
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<213> Corynebacterium glutamicum

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 35 40 45

Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln Thr Ala Asp Leu Val
 50 55 60

Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val Asp Ala Phe Ser Ala
 65 70 75 80

Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly Asn Lys Met Thr Val
 85 90 95

Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe Glu Val Pro Val Gln
 100 105 110

Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu Asn Ile Arg Ala Leu
 115 120 125

Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly Asp Ile Ser Arg Lys
 130 135 140

Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys Lys Arg Met Lys Asn
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Thr Asp Glu Ala
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Met Ala Glu Lys Phe 5															
gca gaa aca aca ttt acg gat cca gcc agg att cgt aac ttc tgc atc 163															
Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile Arg Asn Phe Cys Ile 20															
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Ile Ala His Ile Asp His Gly Lys Ser Thr Leu Ala Asp Arg Ile Leu 35															
cag ctg tct aac gtt gtg gat gcc cgc gat atg cgt gat cag tac ctg 259															
Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met Arg Asp Gln Tyr Leu 50															
gac aac atg gac atc gaa cgt gaa cgt ggc att acc att aag gct cag 307															
Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala Gln 65															
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Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly Glu Tyr Glu Gly Gln 85															
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Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly His Val Asp Phe Thr 100															
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Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu Gly Ala Ile Leu Leu 115															
gtt gat gca gcg cag ggc att gaa gcc cag acc ttg gca aac ttg tat 499															
Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr Leu Ala Asn Leu Tyr 130															
ttg gct atg gaa aac gat ctt gag atc atc cct gtg ctg aac aag att 547															
Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro Val Leu Asn Lys Ile 145															
gac ctt cca gcg gcg gat cca gac aag tac gcg ttg gag atc gcc aac 595															
Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala Leu Glu Ile Ala Asn 165															
att gtg ggt tgt gaa cct gaa gat gtg ttg cgc gtg tcc ggt aaa act 643															
Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg Val Ser Gly Lys Thr 180															
ggc atg ggt gtc cct gag ctt ctg gat aag gtc gtt gaa ctt atc cca 691															

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gca	cct	acc	tct	gaa	ttt	gag	gaa	gac	gcc	cca	gct	cgt	gcg	atg	att	739	
Ala	Pro	Thr	Ser	Glu	Phe	Glu	Glu	Asp	Ala	Pro	Ala	Arg	Ala	Met	Ile		
		200					205					210					
ttc	gac	tct	gtc	tat	gac	acc	tac	cgc	ggc	gtg	gtt	acc	tac	atc	cgc	787	
Phe	Asp	Ser	Val	Tyr	Asp	Thr	Tyr	Arg	Gly	Val	Val	Thr	Tyr	Ile	Arg		
	215					220					225						
atg	atg	gac	ggc	aag	ctg	aca	cct	cgc	caa	aag	atc	aag	atg	atg	tcc	835	
Met	Met	Asp	Gly	Lys	Leu	Thr	Pro	Arg	Gln	Lys	Ile	Lys	Met	Met	Ser		
230					235					240					245		
acc	ggc	gcc	acc	cac	gag	ttg	ctg	gaa	atc	ggc	atc	gtg	agc	ccc	acc	883	
Thr	Gly	Ala	Thr	His	Glu	Leu	Leu	Glu	Ile	Gly	Ile	Val	Ser	Pro	Thr		
				250					255					260			
cct	aaa	aag	tgt	gtg	ggt	ctt	gga	cct	ggc	gag	gtt	ggt	tac	ctg	atc	931	
Pro	Lys	Lys	Cys	Val	Gly	Leu	Gly	Pro	Gly	Glu	Val	Gly	Tyr	Leu	Ile		
			265					270					275				
acc	ggt	gtg	aag	gac	gtg	cgc	caa	tct	aag	gtg	ggc	gat	acc	gtc	acg	979	
Thr	Gly	Val	Lys	Asp	Val	Arg	Gln	Ser	Lys	Val	Gly	Asp	Thr	Val	Thr		
		280					285					290					
tgg	gca	att	cat	gga	gct	gag	cag	cca	ctg	cgc	ggt	tac	cag	gaa	cca	1027	
Trp	Ala	Ile	His	Gly	Ala	Glu	Gln	Pro	Leu	Arg	Gly	Tyr	Gln	Glu	Pro		
	295					300					305						
aca	ccg	atg	gtt	tac	tcg	ggc	ttg	ttc	ccg	att	tcc	caa	gcg	gat	ttc	1075	
Thr	Pro	Met	Val	Tyr	Ser	Gly	Leu	Phe	Pro	Ile	Ser	Gln	Ala	Asp	Phe		
310					315					320					325		
ccc	gac	ttg	cgc	gat	gcg	ctt	gaa	aag	ctg	cag	ctt	aac	gac	gcc	tcc	1123	
Pro	Asp	Leu	Arg	Asp	Ala	Leu	Glu	Lys	Leu	Gln	Leu	Asn	Asp	Ala	Ser		
				330					335					340			
ctc	acg	tac	gaa	ccc	gaa	acg	tcc	gta	gca	ctg	ggc	ttt	ggt	ttc	cga	1171	
Leu	Thr	Tyr	Glu	Pro	Glu	Thr	Ser	Val	Ala	Leu	Gly	Phe	Gly	Phe	Arg		
			345					350					355				
tgt	ggc	ttc	ctc	gga	ctg	ctg	cac	atg	gaa	atc	acc	cgt	gac	cga	ctc	1219	
Cys	Gly	Phe	Leu	Gly	Leu	Leu	His	Met	Glu	Ile	Thr	Arg	Asp	Arg	Leu		
		360					365					370					
gaa	cgt	gag	ttt	ggc	ctt	gat	ctg	att	tct	acc	gcg	cca	tct	gtt	aac	1267	
Glu	Arg	Glu	Phe	Gly	Leu	Asp	Leu	Ile	Ser	Thr	Ala	Pro	Ser	Val	Asn		
	375					380					385						
tac	cgc	gtt	att	gat	gag	gcg	ggc	aag	gaa	ttc	cgc	gtc	cac	aac	cca	1315	
Tyr	Arg	Val	Ile	Asp	Glu	Ala	Gly	Lys	Glu	Phe	Arg	Val	His	Asn	Pro		
390					395					400					405		
tct	gac	tgg	cct	ggc	gga	aag	ctc	agt	gaa	gtt	tac	gag	ccc	atc		1360	
Ser	Asp	Trp	Pro	Gly	Gly	Lys	Leu	Ser	Glu	Val	Tyr	Glu	Pro	Ile			
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<211> 420

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 232

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Ala Asp Arg Ile Leu Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met
          35           40           45

Arg Asp Gln Tyr Leu Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile
          50           55           60

Thr Ile Lys Ala Gln Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly
 65           70           75           80

Glu Tyr Glu Gly Gln Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly
          85           90           95

His Val Asp Phe Thr Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu
          100          105          110

Gly Ala Ile Leu Leu Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr
          115          120          125

Leu Ala Asn Leu Tyr Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro
          130          135          140

Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala
          145          150          155          160

Leu Glu Ile Ala Asn Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg
          165          170          175

Val Ser Gly Lys Thr Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val
          180          185          190

Val Glu Leu Ile Pro Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro
          195          200          205

Ala Arg Ala Met Ile Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val
          210          215          220

Val Thr Tyr Ile Arg Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys
          225          230          235          240

Ile Lys Met Met Ser Thr Gly Ala Thr His Glu Leu Leu Glu Ile Gly
          245          250          255

Ile Val Ser Pro Thr Pro Lys Lys Cys Val Gly Leu Gly Pro Gly Glu
          260          265          270

Val Gly Tyr Leu Ile Thr Gly Val Lys Asp Val Arg Gln Ser Lys Val
          275          280          285

Gly Asp Thr Val Thr Trp Ala Ile His Gly Ala Glu Gln Pro Leu Arg
          290          295          300

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Gly Tyr Gln Glu Pro Thr Pro Met Val Tyr Ser Gly Leu Phe Pro Ile
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 Ser Gln Ala Asp Phe Pro Asp Leu Arg Asp Ala Leu Glu Lys Leu Gln
 325 330 335
 Leu Asn Asp Ala Ser Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu
 340 345 350
 Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile
 355 360 365
 Thr Arg Asp Arg Leu Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr
 370 375 380
 Ala Pro Ser Val Asn Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe
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 Tyr Glu Pro Ile
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 <223> RXA01573

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 Met Lys Arg Leu Ser
 1 5
 cgt gca gcc ctc gca gtg gtc gcc acc acc gca gtt agc ttc agc gca 163
 Arg Ala Ala Leu Ala Val Val Ala Thr Thr Ala Val Ser Phe Ser Ala
 10 15 20
 ctc gca gtt cca gct ttc gca gac gaa gca agc aat gtt gag ctc aac 211
 Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser Asn Val Glu Leu Asn
 25 30 35
 atc ctc ggt gtc acc gac ttc cac gga cac atc gag cag aag gct gtt 259
 Ile Leu Gly Val Thr Asp Phe His Gly His Ile Glu Gln Lys Ala Val
 40 45 50
 aaa gat gat aag gga gta atc acc ggt tac tca gaa atg ggt gcc agt 307
 Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser Glu Met Gly Ala Ser
 55 60 65
 ggc gtt gcc tgc tac gtc gac gct gaa cgc gcg gac aac cca aac acc 355
 Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala Asp Asn Pro Asn Thr

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cgc ttc atc acc gtt ggt gac aac att ggt gga tcc cca ttc gtg tcc				403
Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly Ser Pro Phe Val Ser	90	95	100	
tcc atc ctg aag gat gag cca acc ttg caa gcc ctg agc gcc atc ggt				451
Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala Leu Ser Ala Ile Gly	105	110	115	
gtt gac gca tcc gca ctg ggc aat cac gaa ttc gac cag ggc tac tca				499
Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe Asp Gln Gly Tyr Ser	120	125	130	
gac ctg gtg aac cgc gtt tcc ctg gac ggc tcc ggc agc gca aag ttc				547
Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser Gly Ser Ala Lys Phe	135	140	145	
cca tac ctg ggc gca aac gtt gaa ggt ggc acc cca gca cct gca aag				595
Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr Pro Ala Pro Ala Lys	150	155	160	165
tct gaa atc atc gag atg gac ggc gtc aag atc gct tac gtc ggc gca				643
Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile Ala Tyr Val Gly Ala	170	175	180	
gta acc gag gag acc gca acc ttg gtc tcc cca gca ggc atc gaa ggc				691
Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro Ala Gly Ile Glu Gly	185	190	195	
atc acc ttc acc ggc gac atc gac gct atc aac gca gaa gca gat cgc				739
Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn Ala Glu Ala Asp Arg	200	205	210	
gtc att gag gca ggc gaa gca gac gta gtc atc gca ttg atc cac gct				787
Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile Ala Leu Ile His Ala	215	220	225	
gaa gcc gct cca acc gat cta ttc tcc aac aac gtt gac gtt gta ttc				835
Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn Val Asp Val Val Phe	230	235	240	245
tcc gga cac acc cac ttc gac tac gtt gct gaa ggc gaa gca cgt ggc				883
Ser Gly His Thr His Phe Asp Tyr Val Ala Glu Gly Glu Ala Arg Gly	250	255	260	
gac aag cag cca ctg gtt gtc atc cag ggc cac gaa tac ggc aag gtc				931
Asp Lys Gln Pro Leu Val Val Ile Gln Gly His Glu Tyr Gly Lys Val	265	270	275	
atc tcc gac gtg gag atc tcc tac gac cgc gaa gca ggc aag atc acc				979
Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu Ala Gly Lys Ile Thr	280	285	290	
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Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp Val Val Glu Asn Cys	295	300	305	
gag act cca aac aca gca gtc gac gca atc gtt gca gct gct gtt gag				1075
Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val Ala Ala Val Glu	310	315	320	325

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Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala Thr Ile Asp Asn Gly	
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ttc tac cgt ggg gcg gat gaa gag ggt acg acc ggc tcc aac cgt ggt	1171
Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr Gly Ser Asn Arg Gly	
345 350 355	
gtt gag tct tcc ctg agc aac ctc atc gca gaa gct gga ctg tgg gca	1219
Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu Ala Gly Leu Trp Ala	
360 365 370	
gtc aac gac gcg acc atc ctg aac gct gac atc ggc atc atg aac gca	1267
Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile Gly Ile Met Asn Ala	
375 380 385	
ggc ggc gtg cgt gcg gac ctc gaa gca ggc gaa gtt acc ttc gca gat	1315
Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu Val Thr Phe Ala Asp	
390 395 400 405	
gca tac gca acc cag aac ttc tcc aac acc tac ggc gta cgt gaa gtg	1363
Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr Gly Val Arg Glu Val	
410 415 420	
tct ggt gcg cag ttc aaa gaa gca ctg gaa cag cag tgg aag gaa acc	1411
Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln Gln Trp Lys Glu Thr	
425 430 435	
ggc gac cgc cca cgt ctg gca ttg gga ctg tcc agc aac gtc cag tac	1459
Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser Ser Asn Val Gln Tyr	
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tcc tac gac gag acc cgc gaa tac ggc gac cgc atc acc cac atc acc	1507
Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg Ile Thr His Ile Thr	
455 460 465	
ttc aac ggt gag cca atg gat atg aag gag acc tac cgc gtc aca gga	1555
Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr Tyr Arg Val Thr Gly	
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Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe Thr Ala Phe Ala Glu	
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Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp Ile Asp Leu Phe Asn	
505 510 515	
aac tac atc gca gct cac cca gat gca cca att cgt gca aat cag agc	1699
Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile Arg Ala Asn Gln Ser	
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tca gta ggc atc gcc ctt tcc ggc ccg gca gtt gca gaa gac gga act	1747
Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val Ala Glu Asp Gly Thr	
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Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu Ser Ser Leu Ser Tyr	
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acc gga cct gaa gct aag cca acc acc gtt gag gtg acc gtt ggt act 1843
 Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu Val Thr Val Gly Thr
 570 575 580

gag aag aag act gcg gac gtc gat aac acc atc gtt cct cag ttt gac 1891
 Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile Val Pro Gln Phe Asp
 585 590 595

agc acc ggc aag gca act gtc acc ctg act gtt cct gag gga gct acc 1939
 Ser Thr Gly Lys Ala Thr Val Thr Leu Thr Val Pro Glu Gly Ala Thr
 600 605 610

tct gtc aag atc gca act gac aat ggc act acc ttt gaa ctg cca gta 1987
 Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr Phe Glu Leu Pro Val
 615 620 625

acc gta aac ggt gaa ggc aac aat gat gac gat gat gat aag gag cag 2035
 Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp Asp Asp Lys Glu Gln
 630 635 640 645

cag tcc tcc gga tcc tcc gac gcc ggt tcc ctt gta gca gtt ctc ggt 2083
 Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu Val Ala Val Leu Gly
 650 655 660

gtt ctt gga gca ctc ggt ggc ctg gtg gcg ttc ttc ctg aac tct gcg 2131
 Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe Phe Leu Asn Ser Ala
 665 670 675

cag ggc gca cca ttc ttg gct cag ctt cag gct atg ttt gcg cag ttc 2179
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 Met

<210> 234
 <211> 694
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 234
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Glu Gln Lys Ala Val Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser
 50 55 60

Glu Met Gly Ala Ser Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala
 65 70 75 80

Asp Asn Pro Asn Thr Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly
 85 90 95

Ser Pro Phe Val Ser Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala
 100 105 110
 Leu Ser Ala Ile Gly Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe
 115 120 125
 Asp Gln Gly Tyr Ser Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser
 130 135 140
 Gly Ser Ala Lys Phe Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr
 145 150 155 160
 Pro Ala Pro Ala Lys Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile
 165 170 175
 Ala Tyr Val Gly Ala Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro
 180 185 190
 Ala Gly Ile Glu Gly Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn
 195 200 205
 Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile
 210 215 220
 Ala Leu Ile His Ala Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn
 225 230 235 240
 Val Asp Val Val Phe Ser Gly His Thr His Phe Asp Tyr Val Ala Glu
 245 250 255
 Gly Glu Ala Arg Gly Asp Lys Gln Pro Leu Val Val Ile Gln Gly His
 260 265 270
 Glu Tyr Gly Lys Val Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu
 275 280 285
 Ala Gly Lys Ile Thr Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp
 290 295 300
 Val Val Glu Asn Cys Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val
 305 310 315 320
 Ala Ala Ala Val Glu Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala
 325 330 335
 Thr Ile Asp Asn Gly Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr
 340 345 350
 Gly Ser Asn Arg Gly Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu
 355 360 365
 Ala Gly Leu Trp Ala Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile
 370 375 380
 Gly Ile Met Asn Ala Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu
 385 390 395 400
 Val Thr Phe Ala Asp Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr
 405 410 415
 Gly Val Arg Glu Val Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln

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		450					455					460			
Ile	Thr	His	Ile	Thr	Phe	Asn	Gly	Glu	Pro	Met	Asp	Met	Lys	Glu	Thr
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Tyr	Arg	Val	Thr	Gly	Ser	Ser	Phe	Leu	Leu	Ala	Gly	Gly	Asp	Ser	Phe
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Thr	Ala	Phe	Ala	Glu	Gly	Gly	Pro	Ile	Ala	Glu	Thr	Gly	Met	Val	Asp
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Ile	Asp	Leu	Phe	Asn	Asn	Tyr	Ile	Ala	Ala	His	Pro	Asp	Ala	Pro	Ile
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Arg	Ala	Asn	Gln	Ser	Ser	Val	Gly	Ile	Ala	Leu	Ser	Gly	Pro	Ala	Val
		530					535					540			
Ala	Glu	Asp	Gly	Thr	Leu	Val	Pro	Gly	Glu	Glu	Leu	Thr	Val	Asp	Leu
							550					555			
Ser	Ser	Leu	Ser	Tyr	Thr	Gly	Pro	Glu	Ala	Lys	Pro	Thr	Thr	Val	Glu
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Val	Thr	Val	Gly	Thr	Glu	Lys	Lys	Thr	Ala	Asp	Val	Asp	Asn	Thr	Ile
			580					585						590	
Val	Pro	Gln	Phe	Asp	Ser	Thr	Gly	Lys	Ala	Thr	Val	Thr	Leu	Thr	Val
		595					600							605	
Pro	Glu	Gly	Ala	Thr	Ser	Val	Lys	Ile	Ala	Thr	Asp	Asn	Gly	Thr	Thr
		610					615					620			
Phe	Glu	Leu	Pro	Val	Thr	Val	Asn	Gly	Glu	Gly	Asn	Asn	Asp	Asp	Asp
							630					635			
Asp	Asp	Lys	Glu	Gln	Gln	Ser	Ser	Gly	Ser	Ser	Asp	Ala	Gly	Ser	Leu
				645					650					655	
Val	Ala	Val	Leu	Gly	Val	Leu	Gly	Ala	Leu	Gly	Gly	Leu	Val	Ala	Phe
			660					665						670	
Phe	Leu	Asn	Ser	Ala	Gln	Gly	Ala	Pro	Phe	Leu	Ala	Gln	Leu	Gln	Ala
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<211> 1116

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1093)

<223> RXN01445

<400> 235

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aggcttggga aattttggca tccaggtaat cgcgctgtca atg atc cca ctt att 115
                                         Met Ile Pro Leu Ile
                                         1 5

aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act 163
Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
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gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att 211
Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
                        25 30 35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc 259
Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
                        40 45 50

gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct 307
Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
                        55 60 65

ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa 355
Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
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Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
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Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
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aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca 499
Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
                        120 125 130

aga tcg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag 547
Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
                        135 140 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att 595
Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
                        150 155 160 165

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Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
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gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca 691
Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
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gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat 739
Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
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 215 220 225
 gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc 835
 Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
 230 235 240 245
 tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc 883
 Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
 250 255 260
 ata aca gaa aaa gca cag tct ctt cag att cta gta atg aat cct att 931
 Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu Val Met Asn Pro Ile
 265 270 275
 gga gat tgg cat gca aat ggg gag tcc gca att cca ggt gtg ggc att 979
 Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile Pro Gly Val Gly Ile
 280 285 290
 ggc gta gaa agc tta acc aga agg ata cgt aat att aaa gga cag gtc 1027
 Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn Ile Lys Gly Gln Val
 295 300 305
 tgt gtg act tca ctg caa gga tac tgg aaa gta gtt att tca cta cct 1075
 Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val Val Ile Ser Leu Pro
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<210> 236

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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 Leu Thr Gly Phe Ile Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg
 35 40 45
 Gly Arg Phe Ala Leu Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile
 50 55 60
 Ala Tyr Gly Val Ala Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro
 65 70 75 80
 Ser Leu Ile Thr Glu Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly
 85 90 95
 Ala Gly Arg Trp Lys Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr
 100 105 110

Gln Gln Glu Ile Ile Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu
 115 120 125
 His Asp Ser Met Ala Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys
 130 135 140
 Leu Thr Glu Leu Glu Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn
 145 150 155 160
 Ser Ile Ala Lys Ile Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu
 165 170 175
 Val Arg His Leu Val Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe
 180 185 190
 Gly Ala Trp Ala Ala Val Ser Ile His Asp Thr Val Asn Ser Ala Ile
 195 200 205
 Gln Leu Leu Val Asp Ala Gly His Val Val Ser Phe Asp Ser Arg Lys
 210 215 220
 Lys Asn Tyr Lys Leu Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala
 225 230 235 240
 Phe Asn Glu Ala Val Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala
 245 250 255
 Asn Val Thr Ile Arg Ile Thr Glu Lys Ala Gln Ser Leu Gln Ile Leu
 260 265 270
 Val Met Asn Pro Ile Gly Asp Trp His Ala Asn Gly Glu Ser Ala Ile
 275 280 285
 Pro Gly Val Gly Ile Gly Val Glu Ser Leu Thr Arg Arg Ile Arg Asn
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 Ile Lys Gly Gln Val Cys Val Thr Ser Leu Gln Gly Tyr Trp Lys Val
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 Val Ile Ser Leu Pro Leu Lys Cys Glu Asp Ser
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<210> 237

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXN03143

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 Val Lys Thr Ser Gln
 1 5

gcg acc atc gcc cga att gag aga gtt ctc att tgg gga ttg cat tta 163

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ctc	att	gcc	gtt	ttg	ttg	gtg	ttg	gtg	tgt	tgg	cgt	gcc	agc	cat	tgg	211	
Leu	Ile	Ala	Val	Leu	Leu	Val	Leu	Val	Cys	Trp	Arg	Ala	Ser	His	Trp		
			25					30					35				
ggc	gtg	tgg	gtg	ctc	gct	ttt	ggc	tat	ggc	gtg	gtt	tat	gtg	gcg	ggc	259	
Gly	Val	Trp	Val	Leu	Ala	Phe	Gly	Tyr	Gly	Val	Val	Tyr	Val	Ala	Gly		
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gtg	gtc	ccg	aat	tcg	ccg	ttt	aag	aat	cac	cct	atg	gcg	tgg	ttt	ctt	307	
Val	Val	Pro	Asn	Ser	Pro	Phe	Lys	Asn	His	Pro	Met	Ala	Trp	Phe	Leu		
		55				60					65						
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Val	Leu	Ser	Leu	Leu	Trp	Ala	Ser	Leu	Ile	Trp	Asp	Gly	Pro	Glu	Pro		
	70				75					80					85		
gcg	tat	ttg	gtg	ttt	ccg	atg	ttt	ttc	ctc	gca	gtg	ttg	atc	acg	aca	403	
Ala	Tyr	Leu	Val	Phe	Pro	Met	Phe	Phe	Leu	Ala	Val	Leu	Ile	Thr	Thr		
			90						95					100			
ccg	ctg	aaa	tcc	gcg	atc	atc	att	gca	ata	ctg	acg	gcg	atc	gcg	gtg	451	
Pro	Leu	Lys	Ser	Ala	Ile	Ile	Ile	Ala	Ile	Leu	Thr	Ala	Ile	Ala	Val		
			105					110					115				
gtt	acg	ttg	gct	atg	cac	ctg	ggg	ttt	tct	gtt	ggc	gtt	gtc	acc	ggc	499	
Val	Thr	Leu	Ala	Met	His	Leu	Gly	Phe	Ser	Val	Gly	Val	Val	Thr	Gly		
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ccg	atc	ctt	ggc	gcg	ttg	gtg	gcg	tgg	gta	atg	ggc	acg	tgt	ttt	cag	547	
Pro	Ile	Leu	Gly	Ala	Leu	Val	Ala	Trp	Val	Met	Gly	Thr	Cys	Phe	Gln		
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tta	ttg	gca	caa	gcc	tta	aag	gag	ctt	gtc	gac	gca	cgt	gcg	tcg	gcg	595	
Leu	Leu	Ala	Gln	Ala	Leu	Lys	Glu	Leu	Val	Asp	Ala	Arg	Ala	Ser	Ala		
		150			155					160					165		
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Ile	Arg	Ala	Ser	Lys	Ser	Ala	Gly	Glu	Gln	Ala	Glu	Arg	Ala	Arg	Ile		
				170				175						180			
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Ala	Gly	Glu	Ile	His	Asp	Thr	Val	Ala	Gln	Gly	Leu	Ser	Ser	Ile	Gln		
			185					190					195				
atg	ttg	ttg	cat	gcg	gcg	gaa	aaa	cgg	gtg	gat	gat	ccg	cag	gcg	tta	739	
Met	Leu	Leu	His	Ala	Ala	Glu	Lys	Arg	Val	Asp	Asp	Pro	Gln	Ala	Leu		
		200					205					210					
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Ser	His	Ile	Arg	Leu	Ala	Arg	Gln	Thr	Thr	Ala	Asp	Asn	Leu	Ala	Glu		
		215				220					225						
acc	agg	cag	atc	att	gct	gcg	ctg	caa	ccg	act	cca	ctc	att	ggg	gcg	835	
Thr	Arg	Gln	Ile	Ile	Ala	Ala	Leu	Gln	Pro	Thr	Pro	Leu	Ile	Gly	Ala		
		230			235					240					245		
gat	ctg	ccg	gtg	gcg	ttg	gcc	aga	ctg	tcg	tcg	acc	acc	ccg	atg	gga	883	
Asp	Leu	Pro	Val	Ala	Leu	Ala	Arg	Leu	Ser	Ser	Thr	Thr	Pro	Met	Gly		

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Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro Arg Val Leu Pro Asp																															
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Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln Thr Leu Leu Gly Asn																															
280										285										290											
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Val Val Arg His Ala Gln Ala Asp Ser Ala Lys Met Thr Leu Thr Tyr																															
295										300										305											
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Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp Asn Gly Gln Gly Phe																															
310										315										320										325	
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Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile Gly Leu Pro Thr Ala																															
330										335										340											
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Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile Ile Ile Glu Ser Thr																															
345										350										355											
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Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe Pro Tyr Pro Gln Lys																															
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Asp Gln Asp Lys																															
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<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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Arg Ala Ser His Trp Gly Val Trp Val Leu Ala Phe Gly Tyr Gly Val	
35 40 45	

Val Tyr Val Ala Gly Val Val Pro Asn Ser Pro Phe Lys Asn His Pro	
50 55 60	

Met Ala Trp Phe Leu Val Leu Ser Leu Leu Trp Ala Ser Leu Ile Trp	
65 70 75 80	

Asp Gly Pro Glu Pro Ala Tyr Leu Val Phe Pro Met Phe Phe Leu Ala	
85 90 95	

Val Leu Ile Thr Thr Pro Leu Lys Ser Ala Ile Ile Ile Ala Ile Leu	
100 105 110	

Thr Ala Ile Ala Val Val Thr Leu Ala Met His Leu Gly Phe Ser Val
 115 120 125
 Gly Val Val Thr Gly Pro Ile Leu Gly Ala Leu Val Ala Trp Val Met
 130 135 140
 Gly Thr Cys Phe Gln Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp
 145 150 155 160
 Ala Arg Ala Ser Ala Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala
 165 170 175
 Glu Arg Ala Arg Ile Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly
 180 185 190
 Leu Ser Ser Ile Gln Met Leu Leu His Ala Ala Glu Lys Arg Val Asp
 195 200 205
 Asp Pro Gln Ala Leu Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala
 210 215 220
 Asp Asn Leu Ala Glu Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr
 225 230 235 240
 Pro Leu Ile Gly Ala Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser
 245 250 255
 Thr Thr Pro Met Gly Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro
 260 265 270
 Arg Val Leu Pro Asp Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln
 275 280 285
 Thr Leu Leu Gly Asn Val Val Arg His Ala Gln Ala Asp Ser Ala Lys
 290 295 300
 Met Thr Leu Thr Tyr Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp
 305 310 315 320
 Asn Gly Gln Gly Phe Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile
 325 330 335
 Gly Leu Pro Thr Ala Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile
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 Ile Ile Glu Ser Thr Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe
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 Pro Tyr Pro Gln Lys Asp Gln Asp Lys
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<210> 239

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> RXN03071

<400> 239

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atg ctg gcg cca tgg cag ctc cac aaa gac gac gac atc gtc gcc cgc 48
Met Leu Ala Pro Trp Gln Leu His Lys Asp Asp Asp Ile Val Ala Arg
  1           5           10           15

aac gag cag atc acc gaa gcc ttc gag cgc gac gtc gtc cca tac gcg 96
Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala
          20           25           30

gag ctt ttc gac gcc tcc ggc cag att cct tca tcg cag gag ttc ttc 144
Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe
          35           40           45

cgc gtg tca ctc acc gga cag tat ctt cca gac agt gag gtt ttg ctg 192
Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu
          50           55           60

cgc ctt cgc ccc gtc gac tcc ggc cca gca ttc caa tcg tta acc ccc 240
Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro
          65           70           75           80

ttc gaa ctt gaa aac gga cag att gtc ctc gtc aac cgt ggt tac gaa 288
Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu
          85           90           95

tca tca gag ggc aca atc gtc cca gag atc gag cct gct cct tca cac 336
Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His
          100          105          110

cag taaccatcac cggattcgcc gca 362
Gln

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<210> 240

<211> 113

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

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Met Leu Ala Pro Trp Gln Leu His Lys Asp Asp Asp Ile Val Ala Arg
  1           5           10           15

Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala
          20           25           30

Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe
          35           40           45

Arg Val Ser Leu Thr Gly Gln Tyr Leu Pro Asp Ser Glu Val Leu Leu
          50           55           60

Arg Leu Arg Pro Val Asp Ser Gly Pro Ala Phe Gln Ser Leu Thr Pro
          65           70           75           80

Phe Glu Leu Glu Asn Gly Gln Ile Val Leu Val Asn Arg Gly Tyr Glu
          85           90           95

Ser Ser Glu Gly Thr Ile Val Pro Glu Ile Glu Pro Ala Pro Ser His

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100

105

110

Gln

<210> 241

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN03072

<400> 241

atcagagggc acaatcgctcc cagagatcga gcctgctcct tcacaccagt aaccatcacc 60

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ggattcgccg caagaacgag ggcctccagg ttctgcacct atg gaa gac agc ggc 115
              Met Glu Asp Ser Gly
              1                      5

```

```

tac acc cag gtc tac gga att aac acc gaa cag atc agt gac gtc acc 163
Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln Ile Ser Asp Val Thr
              10                      15                      20

```

```

ggc ctt gat ctt ggc acc gac tac gtc cag gtc gca gaa ggc gaa cct 211
Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val Ala Glu Gly Glu Pro
              25                      30                      35

```

```

ggg gtt ttg aac cca atg cca ctg cct caa atg gac cgc ggt aac cac 259
Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met Asp Arg Gly Asn His
              40                      45                      50

```

```

ctc tca tac ggc ttc cag tgg atc gcc ttc ggc atc atg gca cct tta 307
Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly Ile Met Ala Pro Leu
              55                      60                      65

```

```

ggg ctt gga tac ttc atc tgg gct gaa atg cgc gaa cga cgc cgc gac 355
Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg Glu Arg Arg Arg Asp
              70                      75                      80                      85

```

```

aaa gca gaa cgc gaa cag atg gcc gag cta aac act ctt gaa cca gtg 403
Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn Thr Leu Glu Pro Val
              90                      95                      100

```

```

gtg gaa acc cct gaa gtt gtt gaa act gca gaa cca acc atc acc ccg 451
Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu Pro Thr Ile Thr Pro
              105                      110                      115

```

```

gct gca tcc aaa cga cgt tca cgc tac ggc gat caa cac cgc aat cac 499
Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp Gln His Arg Asn His
              120                      125                      130

```

```

tac gag aag atc tcc aaa cga gac caa gag cgc ttc taagcccgtc 545
Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg Phe
              135                      140                      145

```

```

tcatttttgc acc 558

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<400> 242															
Met 1	Glu	Asp	Ser	Gly 5	Tyr	Thr	Gln	Val	Tyr 10	Gly	Ile	Asn	Thr	Glu 15	Gln
Ile	Ser	Asp	Val 20	Thr	Gly	Leu	Asp	Leu 25	Gly	Thr	Asp	Tyr	Val 30	Gln	Val
Ala	Glu	Gly 35	Glu	Pro	Gly	Val	Leu 40	Asn	Pro	Met	Pro	Leu 45	Pro	Gln	Met
Asp	Arg 50	Gly	Asn	His	Leu	Ser 55	Tyr	Gly	Phe	Gln	Trp 60	Ile	Ala	Phe	Gly
Ile 65	Met	Ala	Pro	Leu 70	Gly	Leu	Gly	Tyr	Phe	Ile 75	Trp	Ala	Glu	Met	Arg 80
Glu	Arg	Arg	Arg	Asp 85	Lys	Ala	Glu	Arg	Glu 90	Gln	Met	Ala	Glu	Leu 95	Asn
Thr	Leu	Glu	Pro 100	Val	Val	Glu	Thr	Pro 105	Glu	Val	Val	Glu	Thr 110	Ala	Glu
Pro	Thr 115	Ile	Thr	Pro	Ala	Ala	Ser 120	Lys	Arg	Arg	Ser	Arg 125	Tyr	Gly	Asp
Gln	His 130	Arg	Asn	His	Tyr	Glu 135	Lys	Ile	Ser	Lys	Arg 140	Asp	Gln	Glu	Arg
Phe 145															

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<220>
<221> CDS
<222> (101)..(577)
<223> RXN01773
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<400> 243
ccctaaaaaac aacgacagca aagctgcggt cggatatatt ctcgaactgc tgtagtgcac 60
acgctacagc ccgctaccac cgtaaaagcg agaacatata atg act gtt gat ctc 115
                                     Met Thr Val Asp Leu
                                     1                               5
tac cag gca cgc att cct ttt cag cgc gat ggc gtg cgc ttt gat cat 163
Tyr Gln Ala Arg Ile Pro Phe Gln Arg Asp Gly Val Arg Phe Asp His
                               10                               15                               20
acg atg atc acc cac att caa gcc ggc ctg cat ctt ggt ggc tgc cgc 211
Thr Met Ile Thr His Ile Gln Ala Gly Leu His Leu Gly Gly Cys Arg

```

25										30					35					
gca	gca	ggt	tta	ctg	cct	ata	cca	gca	cat	att	gat	cat	att	gtg	cgc	259				
Ala	Ala	Gly	Leu	Leu	Pro	Ile	Pro	Ala	His	Ile	Asp	His	Ile	Val	Arg					
		40						45					50							
ctg	aca	gcc	gca	gat	ttc	tat	gac	acc	cag	tca	gca	ccg	cag	ctg	ctc	307				
Leu	Thr	Ala	Ala	Asp	Phe	Tyr	Asp	Thr	Gln	Ser	Ala	Pro	Gln	Leu	Leu					
	55					60					65									
agc	aac	act	gtg	ctt	gat	gta	ttg	gac	acc	acc	act	caa	gac	ttg	aag	355				
Ser	Asn	Thr	Val	Leu	Asp	Val	Leu	Asp	Thr	Thr	Thr	Gln	Asp	Leu	Lys					
	70				75					80					85					
gca	ttg	tgg	cct	ggt	gca	gaa	cat	att	gct	aca	acc	att	cct	gaa	tct	403				
Ala	Leu	Trp	Pro	Val	Ala	Glu	His	Ile	Ala	Thr	Thr	Ile	Pro	Glu	Ser					
				90					95					100						
gag	aac	gtg	ctt	atc	cac	tgc	cag	atg	ggt	atc	aac	cgc	tca	gct	gca	451				
Glu	Asn	Val	Leu	Ile	His	Cys	Gln	Met	Gly	Ile	Asn	Arg	Ser	Ala	Ala					
			105					110					115							
ctc	atg	aca	cgg	gtg	ttg	atg	ttg	cgc	aac	gat	tgc	acc	gcc	gat	gaa	499				
Leu	Met	Thr	Arg	Val	Leu	Met	Leu	Arg	Asn	Asp	Cys	Thr	Ala	Asp	Glu					
		120					125					130								
gca	att	gca	ctg	ctg	cgt	gat	cga	cgc	tca	ccg	ttt	gta	ctg	ttc	aat	547				
Ala	Ile	Ala	Leu	Leu	Arg	Asp	Arg	Arg	Ser	Pro	Phe	Val	Leu	Phe	Asn					
	135					140					145									
gag	cat	ttt	gtg	gaa	caa	ctt	cga	gca	ctg	taagcgcgtca	aagacccatt	acc	600							
Glu	His	Phe	Val	Glu	Gln	Leu	Arg	Ala	Leu											
	150				155															

<210> 244

<211> 159

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Met	Thr	Val	Asp	Leu	Tyr	Gln	Ala	Arg	Ile	Pro	Phe	Gln	Arg	Asp	Gly
1				5					10					15	

Val	Arg	Phe	Asp	His	Thr	Met	Ile	Thr	His	Ile	Gln	Ala	Gly	Leu	His
			20					25					30		

Leu	Gly	Gly	Cys	Arg	Ala	Ala	Gly	Leu	Leu	Pro	Ile	Pro	Ala	His	Ile
		35					40					45			

Asp	His	Ile	Val	Arg	Leu	Thr	Ala	Ala	Asp	Phe	Tyr	Asp	Thr	Gln	Ser
	50					55					60				

Ala	Pro	Gln	Leu	Leu	Ser	Asn	Thr	Val	Leu	Asp	Val	Leu	Asp	Thr	Thr
	65				70					75					80

Thr	Gln	Asp	Leu	Lys	Ala	Leu	Trp	Pro	Val	Ala	Glu	His	Ile	Ala	Thr
				85					90					95	

Thr	Ile	Pro	Glu	Ser	Glu	Asn	Val	Leu	Ile	His	Cys	Gln	Met	Gly	Ile
			100					105					110		

Asn Arg Ser Ala Ala Leu Met Thr Arg Val Leu Met Leu Arg Asn Asp
 115 120 125

Cys Thr Ala Asp Glu Ala Ile Ala Leu Leu Arg Asp Arg Arg Ser Pro
 130 135 140

Phe Val Leu Phe Asn Glu His Phe Val Glu Gln Leu Arg Ala Leu
 145 150 155

<210> 245

<211> 1344

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1321)

<223> RXN03090

<400> 245

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gggacgacga ctaactaacc cctgaggcac tttctatttc atg gct aaa tca act 115
 Met Ala Lys Ser Thr
 1 5

cct ttg att gca tcg cta cgc tgg cga att gtc ctg tgg atg aca gcg 163
 Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val Leu Trp Met Thr Ala
 10 15 20

gtt gtt ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg 211
 Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val
 25 30 35

ctg ctt tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa 259
 Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val Glu Gln Glu
 40 45 50

att gag gag ttt cgt cgc ttt gca gcc gaa gga att gat cca aca act 307
 Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp Pro Thr Thr
 55 60 65

gcg cag cct ttt gag tca ggt cat cgc ctg atg gag gtt tac ctg tcg 355
 Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val Tyr Leu Ser
 70 75 80 85

agg cag att ccg gat gaa aat gaa gcc att gtc ggc att ttc ccc gga 403
 Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile Phe Pro Gly
 90 95 100

gag ctc att cag gtt gat tac tcc cag ctc agt ggc gcc cat ccg ctt 451
 Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala His Pro Leu
 105 110 115

cct ttg gaa cac tcc gat ccg ttg att tcg gaa atc cga cag acc acg 499
 Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg Gln Thr Thr
 120 125 130

ctg aat tct gga gtt ttc agc gat ctt gaa cgc gga acc act cac tgg 547

Leu	Asn	Ser	Gly	Val	Phe	Ser	Asp	Leu	Glu	Arg	Gly	Thr	Thr	His	Trp	
135						140					145					
gga	aag	gtg	aat	ttc	caa	act	gct	tcc	ggt	gag	gcc	gat	ggt	gag	ttc	595
Gly	Lys	Val	Asn	Phe	Gln	Thr	Ala	Ser	Gly	Glu	Ala	Asp	Gly	Glu	Phe	
150					155					160					165	
ggt	gtc	gca	ttc	ttc	gct	gat	aat	ctt	aaa	gac	cag	gtc	aac	ggc	cag	643
Val	Val	Ala	Phe	Phe	Ala	Asp	Asn	Leu	Lys	Asp	Gln	Val	Asn	Gly	Gln	
				170					175					180		
atc	cag	att	ctt	att	ttg	atc	ggc	aca	ggg	ggt	ttg	att	gcc	tca	att	691
Ile	Gln	Ile	Leu	Ile	Leu	Ile	Gly	Thr	Gly	Gly	Leu	Ile	Ala	Ser	Ile	
			185					190					195			
ctg	att	gct	tgg	ttg	att	gcg	ggc	cag	atc	att	gcc	ccg	atc	cgc	aaa	739
Leu	Ile	Ala	Trp	Leu	Ile	Ala	Gly	Gln	Ile	Ile	Ala	Pro	Ile	Arg	Lys	
		200					205					210				
ttg	agt	tcc	gtg	tcc	gca	aag	atc	agt	aat	tcg	gat	ctc	acc	tgg	cgc	787
Leu	Ser	Ser	Val	Ser	Ala	Lys	Ile	Ser	Asn	Ser	Asp	Leu	Thr	Trp	Arg	
	215					220					225					
gtc	cct	gtg	gag	ggt	cgt	gat	gag	att	gcg	cag	ctg	gcc	agg	act	ttt	835
Val	Pro	Val	Glu	Gly	Arg	Asp	Glu	Ile	Ala	Gln	Leu	Ala	Arg	Thr	Phe	
230					235					240					245	
aat	gcc	atg	ttg	gat	cgc	atc	gaa	atc	gcg	tat	aac	gat	cag	cgc	cag	883
Asn	Ala	Met	Leu	Asp	Arg	Ile	Glu	Ile	Ala	Tyr	Asn	Asp	Gln	Arg	Gln	
				250					255					260		
ttc	gtt	gat	gat	gcc	ggc	cac	gag	ctg	cgc	acc	ccg	atc	aca	gtg	gtg	931
Phe	Val	Asp	Asp	Ala	Gly	His	Glu	Leu	Arg	Thr	Pro	Ile	Thr	Val	Val	
			265					270					275			
cgt	ggc	cag	tta	gag	ctt	ctc	gcc	acc	acc	ccg	ccg	gag	gaa	caa	gcg	979
Arg	Gly	Gln	Leu	Glu	Leu	Leu	Ala	Thr	Thr	Pro	Pro	Glu	Glu	Gln	Ala	
		280					285					290				
cgg	tcg	att	gag	ctg	gcc	acc	act	gag	ttg	gat	cga	atg	tcg	cga	atg	1027
Arg	Ser	Ile	Glu	Leu	Ala	Thr	Thr	Glu	Leu	Asp	Arg	Met	Ser	Arg	Met	
	295					300					305					
gtc	aat	gat	ctg	ctc	acc	ctc	gca	gtc	gcc	gat	tct	ggc	acc	ttc	atc	1075
Val	Asn	Asp	Leu	Leu	Thr	Leu	Ala	Val	Ala	Asp	Ser	Gly	Thr	Phe	Ile	
310					315					320					325	
cac	gcc	cac	ccc	acg	gat	gtc	acg	gat	tta	aca	atc	gat	atc	gaa	gac	1123
His	Ala	His	Pro	Thr	Asp	Val	Thr	Asp	Leu	Thr	Ile	Asp	Ile	Glu	Asp	
				330					335					340		
aaa	gcc	cgc	acc	atc	agc	gac	cga	att	ttg	ctt	gtc	gac	gcc	cgc	ccg	1171
Lys	Ala	Arg	Thr	Ile	Ser	Asp	Arg	Ile	Leu	Leu	Val	Asp	Ala	Arg	Pro	
			345					350					355			
agg	gcc	tcg	tca	gcc	tcg	acg	agc	agc	ggg	tca	ccg	agg	cag	tgc	ttg	1219
Arg	Ala	Ser	Ser	Ala	Ser	Thr	Ser	Ser	Gly	Ser	Pro	Arg	Gln	Cys	Leu	
		360					365					370				
gag	ttg	ttc	ggc	aat	gcg	ttg	cgc	tac	agc	gat	gat	gtg	gtg	gag	ttg	1267
Glu	Leu	Phe	Gly	Asn	Ala	Leu	Arg	Tyr	Ser	Asp	Asp	Val	Val	Glu	Leu	

375 380 385
 ggt tca gga ttt caa ggg gtc tgg ccc cca ccg cat ttt tcg cat ttg 1315
 Gly Ser Gly Phe Gln Gly Val Trp Pro Pro Pro His Phe Ser His Leu
 390 395 400 405

 ggt tcg tgacaaagga aacggtgttg ata 1344
 Gly Ser

<210> 246

<211> 407

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

Met Ala Lys Ser Thr Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val
 1 5 10 15

 Leu Trp Met Thr Ala Val Val Phe Leu Thr Leu Ala Ser Val Val Ile
 20 25 30

 Ile Thr Arg Ser Val Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser
 35 40 45

 Ala Val Glu Gln Glu Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly
 50 55 60

 Ile Asp Pro Thr Thr Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met
 65 70 75 80

 Glu Val Tyr Leu Ser Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val
 85 90 95

 Gly Ile Phe Pro Gly Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser
 100 105 110

 Gly Ala His Pro Leu Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu
 115 120 125

 Ile Arg Gln Thr Thr Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg
 130 135 140

 Gly Thr Thr His Trp Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu
 145 150 155 160

 Ala Asp Gly Glu Phe Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp
 165 170 175

 Gln Val Asn Gly Gln Ile Gln Ile Leu Ile Leu Ile Gly Thr Gly Gly
 180 185 190

 Leu Ile Ala Ser Ile Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile
 195 200 205

 Ala Pro Ile Arg Lys Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser
 210 215 220

 Asp Leu Thr Trp Arg Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln
 225 230 235 240

Leu Ala Arg Thr Phe Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr
 245 250 255
 Asn Asp Gln Arg Gln Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr
 260 265 270
 Pro Ile Thr Val Val Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro
 275 280 285
 Pro Glu Glu Gln Ala Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp
 290 295 300
 Arg Met Ser Arg Met Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp
 305 310 315 320
 Ser Gly Thr Phe Ile His Ala His Pro Thr Asp Val Thr Asp Leu Thr
 325 330 335
 Ile Asp Ile Glu Asp Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu
 340 345 350
 Val Asp Ala Arg Pro Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser
 355 360 365
 Pro Arg Gln Cys Leu Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp
 370 375 380
 Asp Val Val Glu Leu Gly Ser Gly Phe Gln Gly Val Trp Pro Pro Pro
 385 390 395 400
 His Phe Ser His Leu Gly Ser
 405

<210> 247
 <211> 351
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(328)
 <223> RXN00617

<400> 247
 tacagcgatg atgtggtgga gttgggttca ggatttcaag gggctctggcc cccaccgcat 60
 ttttcgcatt tgggttcgtg acaaaggaaa cgggtgttgat atg gat gaa caa gaa 115
 Met Asp Glu Gln Glu
 1 5
 gcc ctg ttc gat cgc ttc tcc aga ggc tcc caa aaa aat tca cgg cgt 163
 Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln Lys Asn Ser Arg Arg
 10 15 20
 ccc ggt ggc gct ggc ctg gga tta tcc att gtc aag gcg atc ggc gaa 211
 Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val Lys Ala Ile Gly Glu
 25 30 35
 gcc cac gtc ggc cga gct ttc gtc aat tcc aca cca ggt cta gga tcc 259

Ala His Val Gly Arg Ala Phe Val Asn Ser Thr Pro Gly Leu Gly Ser
40 45 50

att ttc ggc ctg gaa atc ccc gca cca gaa caa tca aag gaa tac acc 307
Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln Ser Lys Glu Tyr Thr
55 60 65

cat gag caa gat cct gct cgc tgaagatgac gccggcatcg cag 351
His Glu Gln Asp Pro Ala Arg
70 75

<210> 248

<211> 76

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Met Asp Glu Gln Glu Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln
1 5 10 15

Lys Asn Ser Arg Arg Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val
20 25 30

Lys Ala Ile Gly Glu Ala His Val Gly Arg Ala Phe Val Asn Ser Thr
35 40 45

Pro Gly Leu Gly Ser Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln
50 55 60

Ser Lys Glu Tyr Thr His Glu Gln Asp Pro Ala Arg
65 70 75

<210> 249

<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(697)

<223> RXN02990

<400> 249

gaagactaag caccagtttt aacaaagcag ggacaatcca cacacttaaa ccatgatgtg 60

gcttggttcct gcttttttcgt caacgaaggg caacaacgcg atg gat atc caa gcc 115
Met Asp Ile Gln Ala
1 5

gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct 163
Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala
10 15 20

cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag 211
His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys
25 30 35

aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca 259
Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Leu Asn Gln Arg Ala

40	45	50	
cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag			307
Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu			
55	60	65	
gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg			355
Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu			
70	75	80	85
ctt gat gat gaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc			403
Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val Arg Gln Arg Ala Ala			
	90	95	100
agg cga gga aaa tct tcg cgt gcg ctg gac cgc gaa ctg cag gaa aaa			451
Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg Glu Leu Gln Glu Lys			
	105	110	115
ggc gtc gac aag caa acg cgt gct gcg gcg ctt gag caa atc gac cag			499
Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu Glu Gln Ile Asp Gln			
	120	125	130
gcc gat gag cgg gac acg gcg cgg gcg gtg gcc gtg aaa aag gcg cgc			547
Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala Val Lys Lys Ala Arg			
	135	140	145
tca gag acc aag att ccg cag gac cgc gcc gac tac gac aaa gcg ctt			595
Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp Tyr Asp Lys Ala Leu			
150	155	160	165
cgg cgc gtg gtt ggt gcg ctg gca cgg cgg gga ttt ccg gct gga atg			643
Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly Phe Pro Ala Gly Met			
	170	175	180
tcc atg gac ctt gcg cgg gaa gcg cta gac gcg cga atc gag gat ttg			691
Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala Arg Ile Glu Asp Leu			
	185	190	195
aaa aac taaaccccg atgggaatca tcc			720
Lys Asn			

<210> 250

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met	Asp	Ile	Gln	Ala	Glu	Lys	Ile	Glu	Lys	Leu	Arg	Lys	Ala	Leu	Asp
1				5					10					15	

Asn	Phe	Glu	Arg	Ala	His	Ala	Arg	Gly	Glu	Ser	Asp	Phe	Phe	Asp	His
			20					25					30		

Glu	Lys	Glu	Glu	Lys	Lys	Ala	Asn	Val	Arg	Arg	Arg	Ala	Leu	Leu	Leu
	35						40					45			

Leu	Asn	Gln	Arg	Ala	Arg	Ser	Val	Asn	Glu	Leu	Ser	Thr	Arg	Leu	Lys
	50					55					60				

Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu
65 70 75 80

Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val
85 90 95

Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg
100 105 110

Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu
115 120 125

Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala
130 135 140

Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp
145 150 155 160

Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly
165 170 175

Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala
180 185 190

Arg Ile Glu Asp Leu Lys Asn
195

<210> 251
<211> 341
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(318)
<223> RXN03100

<400> 251
ctc tac ggc cag gac aaa gtg acc tcc gat ccg atg gaa gct gct tac 48
Leu Tyr Gly Gln Asp Lys Val Thr Ser Asp Pro Met Glu Ala Ala Tyr
1 5 10 15

act agc ctc tac ctc tgg aaa gaa atg gta gag aag gcc gat tcc ttt 96
Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe
20 25 30

gat gtc gcc gca att caa gca gcc gcc gac gga acc act ttt gat gca 144
Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
35 40 45

cca gaa gga acc gtg gtg gtt ggc ggc gat aac cac cac atc tcc aaa 192
Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
50 55 60

aca ccg cgc atc ggt cga atc cgc ccg gat gga ttg atc gac acc att 240
Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
65 70 75 80

tgg gaa acc gat tcc cca gtt gat ccg gac cca tac ttg tct tcc tat 288
Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr

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<210> 252
<211> 106
<212> PRT
<213> Corynebacterium glutamicum
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<210> 253
<211> 525
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(502)  
<223> RXN00031
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<400> 253
cacacatcgc ctcgtcatcc ttagacacgc caaatcttcc tgggtccaccg gagtactcga 60

ccataaacgc ccacttaatc aacgtgggct tcgcgatggc  gtg  gca  gct  ggc  caa      115
                                         Val Ala Ala Gly Gln
                                         1                      5

.

tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat      163
Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp
                        10                      15                      20

gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca      211
Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala
                        25                      30                      35

acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg      259

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Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val
40 45 50

tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc 307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
55 60 65

gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat 355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr
70 75 80 85

ttt ggc atc cgc gat gaa cat ccc ggt tgg gat cag atg gaa gaa aag 403
Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp Gln Met Glu Glu Lys
90 95 100

ttt ccc acc agc gcc att gcg gtg ttg gaa ttt aac acc cct tgg tca 451
Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe Asn Thr Pro Trp Ser
105 110 115

aaa ctt gag aga aac tct gct cgg ttg aca gat ttt gtc att cca cgg 499
Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp Phe Val Ile Pro Arg
120 125 130

ggt tagttctgct tcaattgaac aat 525
Gly

<210> 254

<211> 134

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Val Ala Ala Gly Gln Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His
1 5 10 15

Val Leu Cys Ser Asp Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val
20 25 30

Gln Leu Gly Gly Ala Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile
35 40 45

Tyr Glu Asn Gln Val Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro
50 55 60

Asp Val Val Gly Thr Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu
65 70 75 80

Glu Leu Ala His Tyr Phe Gly Ile Arg Asp Glu His Pro Gly Trp Asp
85 90 95

Gln Met Glu Glu Lys Phe Pro Thr Ser Ala Ile Ala Val Leu Glu Phe
100 105 110

Asn Thr Pro Trp Ser Lys Leu Glu Arg Asn Ser Ala Arg Leu Thr Asp
115 120 125

Phe Val Ile Pro Arg Gly
130

<400> 255																	
atacatctca cccaattccc cataactaga caattgcccc gcaacgactg ataagttctcc 60																	
aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc 115																	
Val Thr Glu Leu Ile 5																	
cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163																	
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val 20																	
gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211																	
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys 35																	
gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259																	
Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg Val Leu Ser Ala Asn 50																	
cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307																	
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu 65																	
aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355																	
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val 85																	
acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403																	
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val 100																	
gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451																	
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His 115																	
gtt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc 499																	
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg 130																	
att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt 547																	
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg 145																	
ggg att tcg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595																	
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val 165																	
ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct 643																	
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala 180																	

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt	691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly	
185 190 195	
ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg	739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr	
200 205 210	
ttg atc act ggt gag gtc att gag atg ctg gcg gct cac gcg ggc aag	787
Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly Lys	
215 220 225	
gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctg	835
Glu Ala Glu Val Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu	
230 235 240 245	
gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg	883
Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu	
250 255 260	
gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct	931
Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro	
265 270 275	
ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc	979
Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr	
280 285 290	
gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag	1027
Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu	
295 300 305	
gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat	1075
Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp	
310 315 320 325	
ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg	1123
Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala	
330 335 340	
aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg	1171
Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met	
345 350 355	
tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctc	1219
Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu	
360 365 370	
tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag	1267
Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys	
375 380 385	
gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg	1315
Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu	
390 395 400 405	
cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa	1363
His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu	
410 415 420	

gac ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 1409
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
 425 430

tttctcgacg ccc 1422

<210> 256

<211> 433

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
 1 5 10 15

Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
 20 25 30

Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45

Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60

Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80

Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95

Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110

Pro Arg Ser Ser His Val Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125

Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
 130 135 140

Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
 145 150 155 160

Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
 165 170 175

Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
 180 185 190

Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
 195 200 205

Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
 210 215 220

Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
 225 230 235 240

Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
 245 250 255

Ala	Leu	Ala	Gly 260	Leu	Asp	Ala	Ser	Val 265	Ile	Asp	Glu	Val	Ala 270	Ala	Ala
Ile	Glu	Leu 275	Thr	Pro	Gly	Ala	Arg 280	Thr	Thr	Ile	Arg	Thr 285	Leu	Asn	Arg
Met	Gly 290	Tyr	Gln	Thr	Ala	Val 295	Val	Ser	Gly	Gly	Phe 300	Ile	Gln	Val	Leu
Glu 305	Gly	Leu	Ala	Glu	Glu 310	Leu	Glu	Leu	Asp	Tyr 315	Val	Arg	Ala	Asn	Thr 320
Leu	Glu	Ile	Val	Asp 325	Gly	Lys	Leu	Thr	Gly 330	Asn	Val	Thr	Gly	Lys 335	Ile
Val	Asp	Arg	Ala 340	Ala	Lys	Ala	Glu	Phe 345	Leu	Arg	Glu	Phe	Ala 350	Ala	Asp
Ser	Gly	Leu 355	Lys	Met	Tyr	Gln	Thr 360	Val	Ala	Val	Gly	Asp 365	Gly	Ala	Asn
Asp 370	Ile	Asp	Met	Leu	Ser	Ala 375	Ala	Gly	Leu	Gly	Val 380	Ala	Phe	Asn	Ala
Lys 385	Pro	Ala	Leu	Lys	Glu 390	Ile	Ala	Asp	Thr	Ser 395	Val	Asn	His	Pro	Phe 400
Leu	Asp	Glu	Val	Leu 405	His	Ile	Met	Gly	Ile 410	Ser	Arg	Asp	Glu	Ile 415	Asp
Leu	Ala	Asp	Gln 420	Glu	Asp	Gly	Thr	Phe 425	His	Arg	Val	Pro	Leu	Thr	Asn

Ala

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<210> 257
<211> 738
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(715)  
<223> RXN00978
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<400> 257
tcctgggtag catgggctta tgagcactga tagccaaaac cctgtaagaa aatcctgcg 60
acagccacat tcttgttccc aagaggtgcg attgaaagcg atg tcc agg tca ccg 115
Met Ser Arg Ser Pro
1 5
ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser
10 15 20
cta act gcg tgg tcg tgg gca gaa gat gat cct ttg tac ctc gca ggt 211
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly
25 30 35

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gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259
 Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val
 40 45 50

tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307
 Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr
 55 60 65

ccc ggc gat gtt att ggt gcg ata gat aca gaa cct cag ccg gca gta 355
 Pro Gly Asp Val Ile Gly Ala Ile Asp Thr Glu Pro Gln Pro Ala Val
 70 75 80 85

gat tcc gct tgg gca ata gaa acc acc tgt gcg ctg ttt ctt cca gca 403
 Asp Ser Ala Trp Ala Ile Glu Thr Thr Cys Ala Leu Phe Leu Pro Ala
 90 95 100

acc gcg ttg gca act gtg att gaa cag cat cca agt ttt gct ttg gcg 451
 Thr Ala Leu Ala Thr Val Ile Glu Gln His Pro Ser Phe Ala Leu Ala
 105 110 115

atg att cgg atg cag cag caa cgt ttg gct aca gcc aga gat cat gaa 499
 Met Ile Arg Met Gln Gln Gln Arg Leu Ala Thr Ala Arg Asp His Glu
 120 125 130

att aac ctg act acg acc aca gtt gag caa cga gta gct att gca gtg 547
 Ile Asn Leu Thr Thr Thr Thr Val Glu Gln Arg Val Ala Ile Ala Val
 135 140 145

aga act ctg gga cga aaa atc ggg caa cga cga ccc gat gga atc ttg 595
 Arg Thr Leu Gly Arg Lys Ile Gly Gln Arg Arg Pro Asp Gly Ile Leu
 150 155 160 165

ctc att caa gtt cga atc cgg cgg gaa gat gtt gcg ggt tta gca ggc 643
 Leu Ile Gln Val Arg Ile Arg Arg Glu Asp Val Ala Gly Leu Ala Gly
 170 175 180

acc acc gtg gaa tct act tct aga gtt ttg gcg cga tta cgt aaa gaa 691
 Thr Thr Val Glu Ser Thr Ser Arg Val Leu Ala Arg Leu Arg Lys Glu
 185 190 195

ggg gtc att gat agc ggt agg gaa tgattgccgt ggatcgatgaa cgg 738
 Gly Val Ile Asp Ser Gly Arg Glu
 200 205

<210> 258

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ser Arg Ser Pro Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu
1 5 10 15

Glu Leu Asp Lys Ser Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro
20 25 30

Leu Tyr Leu Ala Gly Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala
35 40 45

Gly 50	Arg	Val	Arg	Val	Ser	Arg 55	Asp	Thr	Ile	Asp	Gly 60	Lys	Glu	Leu	Thr
Val 65	Asp	Ile	Ala	Thr	Pro 70	Gly	Asp	Val	Ile	Gly 75	Ala	Ile	Asp	Thr	Glu 80
Pro	Gln	Pro	Ala	Val 85	Asp	Ser	Ala	Trp	Ala 90	Ile	Glu	Thr	Thr	Cys 95	Ala
Leu	Phe	Leu	Pro 100	Ala	Thr	Ala	Leu	Ala 105	Thr	Val	Ile	Glu	Gln 110	His	Pro
Ser	Phe 115	Ala	Leu	Ala	Met	Ile 120	Arg	Met	Gln	Gln	Gln 125	Arg	Leu	Ala	Thr
Ala 130	Arg	Asp	His	Glu	Ile 135	Asn	Leu	Thr	Thr	Thr 140	Thr	Val	Glu	Gln	Arg
Val 145	Ala	Ile	Ala	Val	Arg 150	Thr	Leu	Gly	Arg	Lys 155	Ile	Gly	Gln	Arg	Arg 160
Pro	Asp	Gly	Ile 165	Leu	Leu	Ile	Gln	Val	Arg 170	Ile	Arg	Arg	Glu	Asp 175	Val
Ala	Gly	Leu	Ala 180	Gly	Thr	Thr	Val	Glu 185	Ser	Thr	Ser	Arg	Val 190	Leu	Ala
Arg	Leu 195	Arg	Lys	Glu	Gly	Val 200	Ile	Asp	Ser	Gly	Arg	Glu 205			

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<210> 259
<211> 900
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(877)  
<223> RXN01349
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<400> 259																	
agttgtcagc tgggatttgc cgatggtgtt atctttgata tttaccttaa ccccgtttct																60	
aattcacggtt ttctcgttac ccgaaaggaa ttgatcgatt																	
												atg	gcg	aca	tca	cgt	115
												Met	Ala	Thr	Ser	Arg	
												1				5	
cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct																163	
Arg	Asp	Ala	Glu	Asn	Ile	Asp	Gln	Ala	Gly	Ser	Glu	Phe	Ile	Glu	Ser		
				10				15				20					
gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg																211	
Asp	Ser	Gly	His	Thr	Ala	Thr	Pro	Glu	Glu	Val	Val	Ala	Thr	Ala	Leu		
				25				30				35					
aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc																259	
Thr	Phe		Ala	Glu	Asp	Gly	Phe	Ser	Glu	Thr	Lys	Leu	Glu	Lys	Ile		
				40				45				50					
gcg aaq gca tct qgc atg tcc aaq cgc atg atc cac tat cac ttt ggc																307	

Ala	Lys	Ala	Ser	Gly	Met	Ser	Lys	Arg	Met	Ile	His	Tyr	His	Phe	Gly		
55						60					65						
gat	aag	aaa	ggc	ctg	tac	atc	aag	gct	gtt	tcc	tac	gcg	ttg	cga	ttg		355
Asp	Lys	Lys	Gly	Leu	Tyr	Ile	Lys	Ala	Val	Ser	Tyr	Ala	Leu	Arg	Leu		
70					75					80					85		
ctg	cg	cca	gag	gct	gaa	gcg	atg	caa	ctt	gat	tcc	gcg	gta	cca	gtt		403
Leu	Arg	Pro	Glu	Ala	Glu	Ala	Met	Gln	Leu	Asp	Ser	Ala	Val	Pro	Val		
				90					95					100			
gat	ggt	gtc	cg	aaa	atc	gtc	gag	gct	tta	tat	acc	tgc	atc	acc	aag		451
Asp	Gly	Val	Arg	Lys	Ile	Val	Glu	Ala	Leu	Tyr	Thr	Cys	Ile	Thr	Lys		
			105					110					115				
cac	cca	gaa	gca	gtg	cg	ctg	cta	ttg	atg	gaa	aac	ctg	cat	agc	caa		499
His	Pro	Glu	Ala	Val	Arg	Leu	Leu	Leu	Met	Glu	Asn	Leu	His	Ser	Gln		
		120					125					130					
gac	agc	gtg	gat	tcc	acc	gcg	gca	tat	tcc	gat	gaa	tcc	aat	gtg	ctg		547
Asp	Ser	Val	Asp	Ser	Thr	Ala	Ala	Tyr	Ser	Asp	Glu	Ser	Asn	Val	Leu		
	135					140					145						
ctc	aac	ctg	gat	aag	ctg	ctc	atg	ctt	ggc	cag	gat	gcc	ggc	gcc	ttc		595
Leu	Asn	Leu	Asp	Lys	Leu	Leu	Met	Leu	Gly	Gln	Asp	Ala	Gly	Ala	Phe		
150					155					160					165		
cgt	cct	gga	atc	tcc	gca	gaa	gac	gta	ctg	gtt	ctt	att	agc	tcc	ctg		643
Arg	Pro	Gly	Ile	Ser	Ala	Glu	Asp	Val	Leu	Val	Leu	Ile	Ser	Ser	Leu		
				170					175					180			
gcc	tac	ttc	cg	gta	tcc	aac	aag	gtc	acg	ttg	aag	aac	ctc	tac	tcc		691
Ala	Tyr	Phe	Arg	Val	Ser	Asn	Lys	Val	Thr	Leu	Lys	Asn	Leu	Tyr	Ser		
			185					190					195				
ctt	gat	ttg	gaa	tca	gag	gcc	aat	att	gaa	ggc	atg	aag	cg	atc	gtc		739
Leu	Asp	Leu	Glu	Ser	Glu	Ala	Asn	Ile	Glu	Gly	Met	Lys	Arg	Ile	Val		
		200					205					210					
gtt	gac	acg	gtg	ctg	gca	ttc	ttg	acc	tca	aat	att	caa	aat	tct	ggc		787
Val	Asp	Thr	Val	Leu	Ala	Phe	Leu	Thr	Ser	Asn	Ile	Gln	Asn	Ser	Gly		
	215					220					225						
aac	tcc	agc	tac	ctg	gtt	gtt	ggt	ggc	aag	act	gca	gaa	cca	gaa	act		835
Asn	Ser	Ser	Tyr	Leu	Val	Val	Gly	Gly	Lys	Thr	Ala	Glu	Pro	Glu	Thr		
230					235				240						245		
gat	gac	agc	gtc	tac	agc	ttt	gat	acg	gac	gtg	ttc	gaa	aac				877
Asp	Asp	Ser	Val	Tyr	Ser	Phe	Asp	Thr	Asp	Val	Phe	Glu	Asn				
				250					255								
taaagggtat	cgagtagttt	caa															900

<210> 260

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Ala Thr Ser Arg Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser

1	5	10	15
Glu Phe Ile	Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val		
	20	25	30
Val Ala Thr	Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr		
	35	40	45
Lys Leu Glu	Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile		
	50	55	60
His Tyr His	Phe Gly Asp Lys Lys Gly Leu Tyr Ile Lys Ala Val Ser		
	65	70	75
Tyr Ala Leu	Arg Leu Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp		
	85	90	95
Ser Ala Val	Pro Val Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr		
	100	105	110
Thr Cys Ile	Thr Lys His Pro Glu Ala Val Arg Leu Leu Leu Met Glu		
	115	120	125
Asn Leu His	Ser Gln Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp		
	130	135	140
Glu Ser Asn	Val Leu Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln		
	145	150	155
Asp Ala Gly	Ala Phe Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val		
	165	170	175
Leu Ile Ser	Ser Leu Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu		
	180	185	190
Lys Asn Leu	Tyr Ser Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly		
	195	200	205
Met Lys Arg	Ile Val Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn		
	210	215	220
Ile Gln Asn	Ser Gly Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr		
	225	230	235
Ala Glu Pro	Glu Thr Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val		
	245	250	255
Phe Glu Asn			

<210> 261
 <211> 792
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(769)
 <223> RXN00467

<400> 261

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agctgatgga aaagaacttc tcaacattct ccgcaacaga aaactacccg cactggaatc 60

agctccgctg ggacaaaaca gcctggacta aggtgtaatc atg cac atc tca gat 115
                                         Met His Ile Ser Asp
                                         1           5

ctt ccc gat agg tcc cag gac tac ctg aag aca atc tgg gac atc aca 163
Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr Ile Trp Asp Ile Thr
                        10                        15                        20

gaa ctc ctt gat gat caa cca gca gca ctc ggc gat atc gcc gaa aaa 211
Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly Asp Ile Ala Glu Lys
                        25                        30                        35

atg aac cag aaa act cct acc gcc tcc gaa gca atc aaa aag ctg gcg 259
Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala Ile Lys Lys Leu Ala
                        40                        45                        50

gca agg ggc ctg gtc aac cat gaa aaa tat gct ggt gtc acc ctc act 307
Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala Gly Val Thr Leu Thr
                        55                        60                        65

gaa cag ggc aaa acg cta gcc atc gac atg gtg cga cgc cac cgc ctg 355
Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val Arg Arg His Arg Leu
                        70                        75                        80                        85

ctg gaa acc ttc ctc cac gat gtt ttg gga tac acc tgg gac gaa gtc 403
Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr Thr Trp Asp Glu Val
                        90                        95                        100

cac gcc gat gca gac ctg ttg gaa cat gca gcc tct gat cag ctc atc 451
His Ala Asp Ala Asp Leu Leu Glu His Ala Ala Ser Asp Gln Leu Ile
                        105                        110                        115

gaa cgc atc gat gct cac ttg ggt cgt cca cgc aaa gat ccc cac ggc 499
Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg Lys Asp Pro His Gly
                        120                        125                        130

gat ccc ata cca act gcc gaa ggc gtt att gaa gag tct ccc cga acc 547
Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu Glu Ser Pro Arg Thr
                        135                        140                        145

acc ctc gag gca gtt cag cca ggg gag act gtc acg att tcc agg gtc 595
Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val Thr Ile Ser Arg Val
                        150                        155                        160                        165

aaa gac att gat cct gaa ttg ctg cgc tac ctc gcg caa tac aac gtc 643
Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu Ala Gln Tyr Asn Val
                        170                        175                        180

tca cca gga tgc cgg atc acc gtt gcg tcc ggc cca cta gct ggc atg 691
Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly Pro Leu Ala Gly Met
                        185                        190                        195

gtg cat gtc gtt gta gaa ggc acc gac acc agc ttc ccc ctg gcc gaa 739
Val His Val Val Val Glu Gly Thr Asp Thr Ser Phe Pro Leu Ala Glu
                        200                        205                        210

acg caa ctg cca tta att aca gtg cag gac taagcagatt catcataatg gtg 792
Thr Gln Leu Pro Leu Ile Thr Val Gln Asp

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215

220

<210> 262

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met His Ile Ser Asp Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr
1 5 10 15

Ile Trp Asp Ile Thr Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly
20 25 30

Asp Ile Ala Glu Lys Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala
35 40 45

Ile Lys Lys Leu Ala Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala
50 55 60

Gly Val Thr Leu Thr Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val
65 70 75 80

Arg Arg His Arg Leu Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr
85 90 95

Thr Trp Asp Glu Val His Ala Asp Ala Asp Leu Leu Glu His Ala Ala
100 105 110

Ser Asp Gln Leu Ile Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg
115 120 125

Lys Asp Pro His Gly Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu
130 135 140

Glu Ser Pro Arg Thr Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val
145 150 155 160

Thr Ile Ser Arg Val Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu
165 170 175

Ala Gln Tyr Asn Val Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly
180 185 190

Pro Leu Ala Gly Met Val His Val Val Val Glu Gly Thr Asp Thr Ser
195 200 205

Phe Pro Leu Ala Glu Thr Gln Leu Pro Leu Ile Thr Val Gln Asp
210 215 220

<210> 263

<211> 861

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(838)

<223> RXN02954

<400> 263

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aagcttcata tcacttttcc acagcctgaa agaacatact atg tcc gca gct tta 115
Met Ser Ala Ala Leu
1 5

cct cac aca gca gca gat ccc gta cac acc acc cca gcg aaa ccg ctg 163
Pro His Thr Ala Ala Asp Pro Val His Thr Thr Pro Ala Lys Pro Leu
10 15 20

ctc gat cat gtc tta gat tca cta gga cgc agc atc atc agt ggt gaa 211
Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser Ile Ile Ser Gly Glu
25 30 35

atg gaa gcc ggt agc aca ttc aaa ctg caa gac atc ggt gaa aaa ttc 259
Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp Ile Gly Glu Lys Phe
40 45 50

ggt atc tcc cgc acc gtc gcc aga gaa gcc atg cgt gcc tta gag caa 307
Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu Glu Gln
55 60 65

ctt ggg ttg gtg gcc tca tcg aga cga att ggt att aca gtg ctc tcg 355
Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val Leu Ser
70 75 80 85

cac gag cac tgg gct gtc ttt gac aaa gcc att att cgc tgg cgc ctc 403
His Glu His Trp Ala Val Phe Asp Lys Ala Ile Ile Arg Trp Arg Leu
90 95 100

gaa gat gag cgt caa cgt gaa cag caa ctg cag tca ctc acc gaa ctt 451
Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln Ser Leu Thr Glu Leu
105 110 115

cgt att gcc att gaa cca att gct gca cgc agt gtt gcc ctt cat gca 499
Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu His Ala
120 125 130

tcg agc gca gag att gct atc atc ggt gat ctt gct gca cga atg cgt 547
Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu Ala Ala Arg Met Arg
135 140 145

aac ctc ggt gaa gct ggt cgt ggc gca tca caa gaa ttc cta gac gca 595
Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln Glu Phe Leu Asp Ala
150 155 160 165

gat gtg aaa ttt cat gag ctt att ttg cag tat tgc cat aat gag atg 643
Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr Cys His Asn Glu Met
170 175 180

ttc gct gcc atg gca cca ccc ata aaa gct gta cta gtc ggg cgc acc 691
Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val Leu Val Gly Arg Thr
185 190 195

aca ctt ggc ctt caa ccc gat cga cct gcc gaa gaa gtc ttg gac aat 739
Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu Glu Val Leu Asp Asn
200 205 210

cat gat gct ctc gca cac gca cta agt gtt cgt aat gca gac ctc gcc 787

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His Asp Ala Leu Ala His Ala Leu Ser Val Arg Asn Ala Asp Leu Ala
 215 220 225

gaa aaa gca tcc agg agc att ctg aat gag gtg cgc gac gca ctg acc 835
 Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val Arg Asp Ala Leu Thr
 230 235 240 245

tcg taattgccac taaacgagtc act 861
 Ser

<210> 264

<211> 246

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Ser Ala Ala Leu Pro His Thr Ala Ala Asp Pro Val His Thr Thr
 1 5 10 15

Pro Ala Lys Pro Leu Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser
 20 25 30

Ile Ile Ser Gly Glu Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp
 35 40 45

Ile Gly Glu Lys Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met
 50 55 60

Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly
 65 70 75 80

Ile Thr Val Leu Ser His Glu His Trp Ala Val Phe Asp Lys Ala Ile
 85 90 95

Ile Arg Trp Arg Leu Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln
 100 105 110

Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser
 115 120 125

Val Ala Leu His Ala Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu
 130 135 140

Ala Ala Arg Met Arg Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln
 145 150 155 160

Glu Phe Leu Asp Ala Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr
 165 170 175

Cys His Asn Glu Met Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val
 180 185 190

Leu Val Gly Arg Thr Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu
 195 200 205

Glu Val Leu Asp Asn His Asp Ala Leu Ala His Ala Leu Ser Val Arg
 210 215 220

Asn Ala Asp Leu Ala Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val

Arg Asp Ala Leu Thr Ser
245

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<220>  
<221> CDS  
<222> (101)..(457)  
<223> RXN03023
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<210> 266
<211> 119
<212> PRT
<213> Corynebacterium glutamicum
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<400> 266

Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
 1 5 10 15

Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
 20 25 30

Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
 35 40 45

Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
 50 55 60

Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
 65 70 75 80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
 85 90 95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
 100 105 110

Glu Ser Arg Gly Leu Tyr Lys
 115

<210> 267

<211> 843

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(820)

<223> RXN03127

<400> 267

aggtagaaca tctgaaagca cttcagataa gacggatggg gtctgatgga aacgacagtc 60

gatatgatca gaaccatctc cagattagga agtgaacaca atg gaa agc tcc aaa 115
 Met Glu Ser Ser Lys
 1 5

aag act tcg cga tca agg tcc act act caa gaa gca gtg cgc gac att 163
 Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu Ala Val Arg Asp Ile
 10 15 20

aaa aaa tac att cgg gac aac cgg ctg cgt acg gga gac ctt ctt cct 211
 Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr Gly Asp Leu Leu Pro
 25 30 35

tcc gaa gcg ttc tta tgt gag gaa ttg ggt tgt tcc cgt tct gcg atc 259
 Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys Ser Arg Ser Ala Ile
 40 45 50

agg gag gcg atc cgc gcg ctc gtg acc ttg gac atc gtc gag gtt cgc 307
 Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp Ile Val Glu Val Arg
 55 60 65

cac ggc tac ggc act ttc gtg tcc agg atg tcc ctc gag ccc ctg atc 355
 His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser Leu Glu Pro Leu Ile

70	75	80	85	
aac ggg atg gtg ttc cgc acg gtg ttg gac aat gac acc tcg gtg gaa				403
Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn Asp Thr Ser Val Glu	90	95	100	
aac ctt ttc tac gtg gtg gat acc cgc gaa atc ctt gac ctt tca ctt				451
Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile Leu Asp Leu Ser Leu	105	110	115	
ggc gaa gag ctg atc gag gtg ttc acc gac gat gac cgc gag cta ctc				499
Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp Asp Arg Glu Leu Leu	120	125	130	
ctt gat ctg gtg gac aag atg cgc gag cac aac gat cag ggc gaa tcc				547
Leu Asp Leu Val Asp Lys Met Arg Glu His Asn Asp Gln Gly Glu Ser	135	140	145	
ttt gtg gtg gag gat caa aaa ttc cac cga gca ctc cta gcg cga acg				595
Phe Val Val Glu Asp Gln Lys Phe His Arg Ala Leu Leu Ala Arg Thr	155	160	165	
aaa aac ccg ctg att aga gag ctc aac gat gcg ttt tgg cag atc caa				643
Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala Phe Trp Gln Ile Gln	170	175	180	
acc gag gcg cag ccc atg ctc aat ctg gct atg ccc gca gac atc gac				691
Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met Pro Ala Asp Ile Asp	185	190	195	
gaa acc atc aaa gct cac agc gac atc gtc gaa gcg ctc tcc agc ggc				739
Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu Ala Leu Ser Ser Gly	200	205	210	
aac atc gac gat tat cgc agc gcc gtg ctc gct cac tac gcg ccg ttt				787
Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala His Tyr Ala Pro Phe	215	220	225	
cgc cgc atg att tcc aac atg ctc gat gcg cac tagcctcatt gcgcgcgggt				840
Arg Arg Met Ile Ser Asn Met Leu Asp Ala His	230	235	240	
tgt				843

<210> 268

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met	Glu	Ser	Ser	Lys	Lys	Thr	Ser	Arg	Ser	Arg	Ser	Thr	Thr	Gln	Glu
1				5					10					15	

Ala	Val	Arg	Asp	Ile	Lys	Lys	Tyr	Ile	Arg	Asp	Asn	Arg	Leu	Arg	Thr
			20					25					30		

Gly	Asp	Leu	Leu	Pro	Ser	Glu	Ala	Phe	Leu	Cys	Glu	Glu	Leu	Gly	Cys
		35					40					45			

Ser	Arg	Ser	Ala	Ile	Arg	Glu	Ala	Ile	Arg	Ala	Leu	Val	Thr	Leu	Asp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ile Val Glu Val Arg His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser 65 70 75 80		
Leu Glu Pro Leu Ile Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn 85 90 95		
Asp Thr Ser Val Glu Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile 100 105 110		
Leu Asp Leu Ser Leu Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp 115 120 125		
Asp Arg Glu Leu Leu Leu Asp Leu Val Asp Lys Met Arg Glu His Asn 130 135 140		
Asp Gln Gly Glu Ser Phe Val Val Glu Asp Gln Lys Phe His Arg Ala 145 150 155 160		
Leu Leu Ala Arg Thr Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala 165 170 175		
Phe Trp Gln Ile Gln Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met 180 185 190		
Pro Ala Asp Ile Asp Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu 195 200 205		
Ala Leu Ser Ser Gly Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala 210 215 220		
His Tyr Ala Pro Phe Arg Arg Met Ile Ser Asn Met Leu Asp Ala His 225 230 235 240		

<210> 269

<211> 1691

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1668)

<223> RXN03155

<400> 269

gga tac cca cca ccg ccc acc gcc tca aaa gac gct gcg ggt ggg ttg Gly Tyr Pro Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu 1 5 10 15	48
cca caa ctg atc aga gag ctt ctc gac gcg acc ccc atc gat cat tgg Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp 20 25 30	96
tcc aac gat cgg cct act ctc acg ctg cca gag cat tgg gtg aca gac Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp 35 40 45	144
atc gac att aag aac cct gtg ctt cgg gaa gtc gcc tcc cat ccc ttc Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe	192

50	55	60	
ttc gat ggc tgc ccg atc gga gat tta gat gcc gat gcc ttt gtg gag Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu 65 70 75 80			240
gat ggc acc ctc att cac gaa aac ggg act tta aga ttc cgc agc cct Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro 85 90 95			288
gag gaa cgc acc ttg gtt cgg gct tct act ccc cca tcg atg gca aga Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg 100 105 110			336
agc ccg cgg gag tgg gaa tcg acg gag gga ggc gtc gat aag cta att Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile 115 120 125			384
gcc gca gga aac ctg ccc ctg gcc cga ctg cat gta gag gaa cta ccc Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro 130 135 140			432
cgt gcc gat gag cag cgc gca ttt ttg gcg ctg tac ggc ggg cag tcg Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser 145 150 155 160			480
ttt gag gcg gcc tcg gcg tcg ccg ttt tat gcg ctg gcc acc tgg aat Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn 165 170 175			528
ccg gag gcg ttg cgg ggc gat ccg acc ttc gat atg ttc gcc gat gcg Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala 180 185 190			576
cta gac act ggg cat tac agg gaa gtc ccg cgt ccg gat gcc cct gaa Leu Asp Thr Gly His Tyr Arg Glu Val Pro Arg Pro Asp Ala Pro Glu 195 200 205			624
gaa agc cag atc cac gat ttc atc agt ggc tgg ctg gcg ttg gtt tac Glu Ser Gln Ile His Asp Phe Ile Ser Gly Trp Leu Ala Leu Val Tyr 210 215 220			672
gat gat ccc ctc acc gcc cgc cgt ctg ctc tcc agt agg ggc ccc tcc Asp Asp Pro Leu Thr Ala Arg Arg Leu Leu Ser Ser Arg Gly Pro Ser 225 230 235 240			720
gat ttg gtg gga ctg tgg cag tcg gcg ttt ttg gcg cga gcg cac tac Asp Leu Val Gly Leu Trp Gln Ser Ala Phe Leu Ala Arg Ala His Tyr 245 250 255			768
gtg ctg gga gaa ttc caa gaa gcc tcc gcc gtt gtc gaa cgc ggc cta Val Leu Gly Glu Phe Gln Glu Ala Ser Ala Val Val Glu Arg Gly Leu 260 265 270			816
gcc acc ggc gac cgc acc gga gcc tcc cta ctc gaa ccc gtg cac ctg Ala Thr Gly Asp Arg Thr Gly Ala Ser Leu Leu Glu Pro Val His Leu 275 280 285			864
tgg acc ggc gcc caa gtc gca gcc atg act ggg cgc acc gaa ttg gcc Trp Thr Gly Ala Gln Val Ala Ala Met Thr Gly Arg Thr Glu Leu Ala 290 295 300			912

aac cac tat tta cag cgc ctg acc gtg ccc gac gat gcg ttc ctc atc	960
Asn His Tyr Leu Gln Arg Leu Thr Val Pro Asp Asp Ala Phe Leu Ile	
305 310 315 320	
caa aaa ctc agc gca tcc atg ggc aaa ttg atc acc gca tcc atg acc	1008
Gln Lys Leu Ser Ala Ser Met Gly Lys Leu Ile Thr Ala Ser Met Thr	
325 330 335	
tca gac acc cgc gca gca acc ttg gcc ggc gac cgc atg gcg tcg gtc	1056
Ser Asp Thr Arg Ala Ala Thr Leu Ala Gly Asp Arg Met Ala Ser Val	
340 345 350	
gta tac acc acc aat acc cag cag ccc gga ttt tgg gcc tgg gaa gac	1104
Val Tyr Thr Thr Asn Thr Gln Gln Pro Gly Phe Trp Ala Trp Glu Asp	
355 360 365	
atg tat gcg atc tca ttg atc cga acg gga cgc atc gac gcc gca gcc	1152
Met Tyr Ala Ile Ser Leu Ile Arg Thr Gly Arg Ile Asp Ala Ala Ala	
370 375 380	
gcc gtc atg gat ggc atc cct gac tcc acc atc ccc tcg ctg cgt gcc	1200
Ala Val Met Asp Gly Ile Pro Asp Ser Thr Ile Pro Ser Leu Arg Ala	
385 390 395 400	
cga aat ttg gtg ccc caa gca aac atc gaa atc caa cga ggc tcc aca	1248
Arg Asn Leu Val Pro Gln Ala Asn Ile Glu Ile Gln Arg Gly Ser Thr	
405 410 415	
gca cga ggc gta aaa atg ctc tcc gaa gcc gtc gac ctc att tcc tcc	1296
Ala Arg Gly Val Lys Met Leu Ser Glu Ala Val Asp Leu Ile Ser Ser	
420 425 430	
gtc aac atg cca gca tat gaa gcc cgc atc ctc ttc gaa tac ggg ctg	1344
Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu	
435 440 445	
gtt cta cga cgc atg ggc agg cgc agc caa gca gcc gaa atg ttc acc	1392
Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr	
450 455 460	
cac gcc gaa gaa gtc ttc acc gcc atg ggt gcg gtc act ctg gct gcc	1440
His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala	
465 470 475 480	
cgc tgc cac ggc gaa cga cga gtc gca ggc gtt ggg cca cgc aga tca	1488
Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser	
485 490 495	
gcg cag gga ctc acc cct caa gag gaa caa atc act gcg ctg gtt gtc	1536
Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val	
500 505 510	
gac ggc tgc tcc aac caa gaa gtc gcc cgt gag ctt tcc ctc tcc gcc	1584
Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala	
515 520 525	
aaa acg gtg gaa tat cac ctc acg agg gtg tac aaa aag ctc ggg gtg	1632
Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val	
530 535 540	

agc tcc cgt gga gag ctt cga gaa tta ctg aag gtc tgacacagcg 1678
 Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val
 545 550 555

ttgttcagca gct 1691

<210> 270

<211> 556

<212> PRT

<213> Corynebacterium glutamicum

<400> 270

Gly Tyr Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu
 1 5 10 15

Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
 20 25 30

Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
 35 40 45

Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
 50 55 60

Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu
 65 70 75 80

Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro
 85 90 95

Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg
 100 105 110

Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile
 115 120 125

Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro
 130 135 140

Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser
 145 150 155 160

Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn
 165 170 175

Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala
 180 185 190

Leu Asp Thr Gly His Tyr Arg Glu Val Pro Arg Pro Asp Ala Pro Glu
 195 200 205

Glu Ser Gln Ile His Asp Phe Ile Ser Gly Trp Leu Ala Leu Val Tyr
 210 215 220

Asp Asp Pro Leu Thr Ala Arg Arg Leu Leu Ser Ser Arg Gly Pro Ser
 225 230 235 240

Asp Leu Val Gly Leu Trp Gln Ser Ala Phe Leu Ala Arg Ala His Tyr
 245 250 255

Val Leu Gly Glu Phe Gln Glu Ala Ser Ala Val Val Glu Arg Gly Leu
260 265 270

Ala Thr Gly Asp Arg Thr Gly Ala Ser Leu Leu Glu Pro Val His Leu
275 280 285

Trp Thr Gly Ala Gln Val Ala Ala Met Thr Gly Arg Thr Glu Leu Ala
290 295 300

Asn His Tyr Leu Gln Arg Leu Thr Val Pro Asp Asp Ala Phe Leu Ile
305 310 315 320

Gln Lys Leu Ser Ala Ser Met Gly Lys Leu Ile Thr Ala Ser Met Thr
325 330 335

Ser Asp Thr Arg Ala Ala Thr Leu Ala Gly Asp Arg Met Ala Ser Val
340 345 350

Val Tyr Thr Thr Asn Thr Gln Gln Pro Gly Phe Trp Ala Trp Glu Asp
355 360 365

Met Tyr Ala Ile Ser Leu Ile Arg Thr Gly Arg Ile Asp Ala Ala Ala
370 375 380

Ala Val Met Asp Gly Ile Pro Asp Ser Thr Ile Pro Ser Leu Arg Ala
385 390 395 400

Arg Asn Leu Val Pro Gln Ala Asn Ile Glu Ile Gln Arg Gly Ser Thr
405 410 415

Ala Arg Gly Val Lys Met Leu Ser Glu Ala Val Asp Leu Ile Ser Ser
420 425 430

Val Asn Met Pro Ala Tyr Glu Ala Arg Ile Leu Phe Glu Tyr Gly Leu
435 440 445

Val Leu Arg Arg Met Gly Arg Arg Ser Gln Ala Ala Glu Met Phe Thr
450 455 460

His Ala Glu Glu Val Phe Thr Ala Met Gly Ala Val Thr Leu Ala Ala
465 470 475 480

Arg Cys His Gly Glu Arg Arg Val Ala Gly Val Gly Pro Arg Arg Ser
485 490 495

Ala Gln Gly Leu Thr Pro Gln Glu Glu Gln Ile Thr Ala Leu Val Val
500 505 510

Asp Gly Cys Ser Asn Gln Glu Val Ala Arg Glu Leu Ser Leu Ser Ala
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Lys Thr Val Glu Tyr His Leu Thr Arg Val Tyr Lys Lys Leu Gly Val
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Ser Ser Arg Gly Glu Leu Arg Glu Leu Leu Lys Val
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<222> (101)..(751)

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                                         Val Asp Ile Glu Glu
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cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163
Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
                        10                               15                               20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211
Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
                        25                               30                               35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259
Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
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ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307
Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
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aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355
Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
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gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc 403
Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
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aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga 451
Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
                        105                               110                               115

cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc 499
Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
                        120                               125                               130

gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag 547
Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
                        135                               140                               145

tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat 595
Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
                        150                               155                               160                               165

cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa 643
Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln
                        170                               175                               180

ggg tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc 691
Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe
                        185                               190                               195

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caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt 739
 Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly
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gga ttt tca gaa tgacatcaca ggtcaagccg gac 774
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<213> Corynebacterium glutamicum

<400> 272

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 35 40 45

Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala
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Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe
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Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val
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Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly
 100 105 110

Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu
 115 120 125

Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu
 130 135 140

His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu
 145 150 155 160

Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile
 165 170 175

Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly
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Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr
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Phe Leu Leu Arg Gly Gly Phe Ser Glu
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Ile	Asp	Gln	Arg	Val	Pro	Ser	Thr	Asn	Glu	Leu	Ala	Ala	Phe	His	Arg	
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Gly	Ile	Leu	Tyr	Lys	Lys	Arg	Gly	Ile	Gly	Met	Phe	Val	Ser	Ala	Gln	
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Ala	Pro	Ala	Leu	Ile	Arg	Glu	Arg	Arg	Asp	Ala	Ala	Phe	Ala	Ala	Thr	
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Tyr	Val	Ala	Pro	Leu	Ile	Asp	Glu	Ser	Ile	His	Leu	Gly	Phe	Thr	Arg	
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Tyr	Lys				

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<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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Ala	Ala	Phe	His	Arg	Ile	Asn	Pro	Ala	Thr	Ala	Arg	Asn	Gly	Leu	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35					40					45					
Leu	Leu	Val	Glu	Ala	Gly	Ile	Leu	Tyr	Lys	Lys	Arg	Gly	Ile	Gly	Met
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Phe	Val	Ser	Ala	Gln	Ala	Pro	Ala	Leu	Ile	Arg	Glu	Arg	Arg	Asp	Ala
65					70					75					80
Ala	Phe	Ala	Ala	Thr	Tyr	Val	Ala	Pro	Leu	Ile	Asp	Glu	Ser	Ile	His
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Leu	Gly	Phe	Thr	Arg	Ala	Arg	Ile	His	Ala	Leu	Leu	Asp	Gln	Val	Ala
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<222> (101)..(787)

<223> RXN00049

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                                     1 5
cag cac aag gac gct tca aca gca caa acc gac aac cag gta cca act 163
Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp Asn Gln Val Pro Thr
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ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act 211
Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
                25                30                35
tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata 259
Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
                40                45                50
gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac 307
Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
                55                60                65
tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc 355
Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
                70                75                80                85
ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac 403
Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
                90                95                100
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Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His

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cta ctt cat ggt tta gaa act ggc cga ttc acc atc gaa gat ctg gac Leu Leu His Gly Leu Glu Thr Gly Arg Phe Thr Ile Glu Asp Leu Asp 150 155 160 165			595
cta gca acc aca tgc act ttt ggt tca ctc atc gca gcg atc caa atg Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile Ala Ala Ile Gln Met 170 175 180			643
gcg ctt tct gca gat caa gat tcc aac gat gac aaa gat cag att ttc Ala Leu Ser Ala Asp Gln Asp Ser Asn Asp Asp Lys Asp Gln Ile Phe 185 190 195			691
gca gcc gcg atg ctc cgg atg gtg ggt gtt caa gca gca gaa gcc cgg Ala Ala Ala Met Leu Arg Met Val Gly Val Gln Ala Ala Glu Ala Arg 200 205 210			739
gag atc gct tcg cgt cca ctc ccc gaa ata tcc cca gtc aaa ccg cag Glu Ile Ala Ser Arg Pro Leu Pro Glu Ile Ser Pro Val Lys Pro Gln 215 220 225			787
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Ala Arg Leu Ile Thr Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val 35 40 45			
Asp Asn Val Gly Ile Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr 50 55 60			
Gly Thr Phe Tyr Asn Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala 65 70 75 80			
Val Ala Glu Asp Ala Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val 85 90 95			
Leu Thr Lys Leu Asp Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg 100 105 110			
His Leu Val Arg His Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe			

115	120	125
Ile Gln Met Gly Ala Ala His Pro Val Leu Met Arg Ile Leu Gly Pro 130 135 140		
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Ile Glu Asp Leu Asp Leu Ala Thr Thr Cys Thr Phe Gly Ser Leu Ile 165 170 175		
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 <223> RXN00486

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 Val Leu Asn Leu Asn
 1 5

cgc tta cac atc ctg cag gaa ttc cac cgc ctg gga acg att aca gca 163
 Arg Leu His Ile Leu Gln Glu Phe His Arg Leu Gly Thr Ile Thr Ala
 10 15 20

gtg gcg gaa tcc atg aac tac agc cgc tct gcc atc tcc caa caa atg 211
 Val Ala Glu Ser Met Asn Tyr Ser Arg Ser Ala Ile Ser Gln Gln Met
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gcg ctg ctg gaa aaa gaa att ggt gtg aaa ctc ttt gaa aaa agc ggc 259
 Ala Leu Leu Glu Lys Glu Ile Gly Val Lys Leu Phe Glu Lys Ser Gly
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cga aac ctc tac ttc aca gaa caa ggc gaa gtg ttg gcc tca gaa aca 307
 Arg Asn Leu Tyr Phe Thr Glu Gln Gly Glu Val Leu Ala Ser Glu Thr
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 His Ala Ile Met Ala Ala Val Asp His Ala Arg Ala Ala Val Leu Asp
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Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys	
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Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala	
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ctc gaa gaa ctc cgc gcc cgc cgc gtc gac gtc gca ctc ggc gag gaa	547
Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu	
135 140 145	
tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc	595
Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val	
150 155 160 165	
ctc ttc gaa gac ccc atg ctg ctc gtc acc cca gca agc ggc cca tac	643
Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr	
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tct ggc ctc acc ctg cca gaa ctc cgc gac atc ccc atc gcc atc gat	691
Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp	
185 190 195	
cca ccc gac ctt ccc gcg ggc gaa tgg gtc cat agg ctc tgc cgg cgc	739
Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg	
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gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctc	787
Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu	
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Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr	
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His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys	
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<212> PRT

<213> Corynebacterium glutamicum

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Ile	Ser	Gln	Gln	Met	Ala	Leu	Leu	Glu	Lys	Glu	Ile	Gly	Val	Lys	Leu
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Phe	Glu	Lys	Ser	Gly	Arg	Asn	Leu	Tyr	Phe	Thr	Glu	Gln	Gly	Glu	Val
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Leu	Ala	Ser	Glu	Thr	His	Ala	Ile	Met	Ala	Ala	Val	Asp	His	Ala	Arg
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Ala	Ala	Val	Leu	Asp	Ser	Leu	Ser	Glu	Val	Ser	Gly	Thr	Leu	Lys	Val
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Thr	Ser	Phe	Gln	Ser	Leu	Leu	Phe	Thr	Leu	Ala	Pro	Lys	Ala	Ile	Ala
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Glu	Gly	Arg	Gln	Gly	His	Pro	Ala	Ile	Lys	Ala	Phe	Arg	Arg	Ala	Leu
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Met Thr Pro Ala Asn 1 5																
gaa agt cct atg act aat cca tta ggt tct gcc ccc acc cca gcc aag 163																
Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala Pro Thr Pro Ala Lys 10 15 20																
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Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu Met Asp Ile Gly Glu 40 45 50																
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Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu Arg Tyr Cys His Asn 170 175 180																
gag atg ttc gct gca ctg att ccg tcg att agc gcg gtt ctt gtc ggc 691																

Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser Ala Val Leu Val Gly
 185 190 195
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 Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro Ala His Glu Ala Leu
 200 205 210
 gac aac cac gat aag ctt gcc gac gcc ctc ctt aac cgc gac gcc gac 787
 Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu Asn Arg Asp Ala Asp
 215 220 225
 gcc gca gaa act gcg tcc cga aac atc ctc aat gag gtg cgc agc gcg 835
 Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn Glu Val Arg Ser Ala
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 <213> Corynebacterium glutamicum

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 Ala Met Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg
 65 70 75 80
 Ile Gly Ile Thr Val Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys
 85 90 95
 Ser Ile Ile Arg Trp Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln
 100 105 110
 Leu Gln Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala
 115 120 125
 Arg Ser Val Ala Leu His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg
 130 135 140
 Ala Leu Ala Thr Glu Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala
 145 150 155 160
 Ser Gln Arg Phe Leu Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu
 165 170 175
 Arg Tyr Cys His Asn Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser
 180 185 190

Ala Val Leu Val Gly Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro
195 200 205

Ala His Glu Ala Leu Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu
210 215 220

Asn Arg Asp Ala Asp Ala Ala Glu Thr Ala Ser Arg Asn Ile Leu Asn
225 230 235 240

Glu Val Arg Ser Ala Leu Gly Thr Leu Asn
245 250

<210> 281

<211> 998

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(975)

<223> RXN01160

<400> 281

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1 5 10 15

ccg tat ttc acc agg tat aaa ggc cgt acc gtc atg gaa gca gcg cgc 96
Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg
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gat ctt ggc caa ccc tcc tcc caa atc atg gaa gac ctc aac aga tta 144
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
35 40 45

tgg atg tgt ggt ctg cca gga ctt ctt cca ggt gac ttg gtg gag ctt 192
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
50 55 60

gat cat tcc ttt aag gaa gta aaa atc cac aat gct caa ggc atg gat 240
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
65 70 75 80

aaa ccc ttg cgc ctc aca cca act gaa gcc ggt gtt ttg ctg ctg aca 288
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
85 90 95

ctt gaa tcc ctg gaa tcc ctc ccc ggt att gcg aaa cag gaa gcg gtc 336
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
100 105 110

gta tct gct gcg aac aag cta cgc gcc atc atg ggg gag tat tcc tcg 384
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
115 120 125

act gtt ttc gac tcc act gga gaa gac ctc gat gct gaa gtt cta gag 432
Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
130 135 140

atc atc cgc gac gcc atg gat tta cac cag cag gtc agt ttt gaa tac 480
 Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
 145 150 155 160
 cac tcg cac aga tca gac aac acc agc ctg agg caa gtc agc cct gct 528
 His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
 165 170 175
 cat atc ttc acc cat gaa ggc gaa acc tac atc aaa gcc tgg gaa gaa 576
 His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
 180 185 190
 gct gtg aac caa tgg cgg acg ttt agg ctt gat cgc atc cga agc att 624
 Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
 195 200 205
 gtg ctt ctt gac agc aaa gca gtg cac ccg gcg cga ggg gtt tca gta 672
 Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
 210 215 220
 tcc acg gac gat cct ttt gag ttc gca aaa tct tcc gat att gcc acg 720
 Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
 225 230 235 240
 tta ttg ctg cgt gag gac gca atg tgg tta ggc aat tac atg gcc atg 768
 Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
 245 250 255
 gag gtg gat gaa acg gtg gaa ccg att cgc gat agc gac gga ttc agc 816
 Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
 260 265 270
 tgg cac aca gtc cac ttt ccg ctg ctt tct agg gat tgg ttc gtc cga 864
 Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
 275 280 285
 ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat 912
 Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
 290 295 300
 ctt ccg aaa tgc ata aag caa aag gct ttt agt ggt ttg tca gcg tat 960
 Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
 305 310 315 320
 gat cat cac gta gag taacacccaa gagtaagacg caa 998
 Asp His His Val Glu
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<210> 282

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

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Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu
 35 40 45
 Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu
 50 55 60
 Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp
 65 70 75 80
 Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr
 85 90 95
 Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val
 100 105 110
 Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser
 115 120 125
 Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu
 130 135 140
 Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr
 145 150 155 160
 His Ser His Arg Ser Asp Asn Thr Ser Leu Arg Gln Val Ser Pro Ala
 165 170 175
 His Ile Phe Thr His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu
 180 185 190
 Ala Val Asn Gln Trp Arg Thr Phe Arg Leu Asp Arg Ile Arg Ser Ile
 195 200 205
 Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val
 210 215 220
 Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr
 225 230 235 240
 Leu Leu Leu Arg Glu Asp Ala Met Trp Leu Gly Asn Tyr Met Ala Met
 245 250 255
 Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser
 260 265 270
 Trp His Thr Val His Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg
 275 280 285
 Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp
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 Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr
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 Asp His His Val Glu
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<210> 283

<211> 3495

<212> DNA

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<222> (101) .. (3472)

<223> RXN02097

<400> 283

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Met Pro Ala Gly Ile
1 5

gca gac atg aca gat tca ttg ctc gga tgg gca tca caa act gag ctg 163
Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala Ser Gln Thr Glu Leu
10 15 20

gat ctg aac cag cgt ctt gca ggg gta gag tac ttt cca caa att cag 211
Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
25 30 35

ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt 259
Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
40 45 50

ttg tcc cgc cag gta ggc gcg ggc gca agc ctt ggg gat ctt ttt gaa 307
Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
55 60 65

atg acc cca tgc ctg aca gtc acc acc ttg gtg tct cgg gcg tca cgg 355
Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg
70 75 80 85

atc agc gat cca gca gat ttc ttc ggt gaa tac atc gga gga ctg gga 403
Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly
90 95 100

ctt agc gca gaa cac gca gca gtt gtt gaa ggg ttg acc gaa aag ctc 451
Leu Ser Ala Glu His Ala Ala Val Val Glu Gly Leu Thr Glu Lys Leu
105 110 115

ttc gca cag gct ggc ctg ctc gtt cct gag gga att gca tct cca ttg 499
Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu
120 125 130

gag ttg tta tcc atc cac gca ggc att agt aac cac gaa gtg gcc gca 547
Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn His Glu Val Ala Ala
135 140 145

gtg	ctg	acc	gaa	gtg	gaa	aac	ggc	acc	acc	gaa	tat	cca	ttc	atg	ttc	595
Val	Leu	Thr	Glu	Val	Glu	Asn	Gly	Thr	Thr	Glu	Tyr	Pro	Phe	Met	Phe	
150					155					160					165	

gac gct gtc ctg cgc cta acc cct gag tgg gca cag acc ctt atc ggc 643
Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala Gln Thr Leu Ile Gly
170 175 180

gga gtt caa gaa ctc att gaa ttt gcc acc acc cac cga act tct tgg 691
Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr His Arg Thr Ser Trp
185 190 195

tca gac cgc cag cgc gaa tcc tca ctg cca gcc atg atc gat gag atc	739
Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala Met Ile Asp Glu Ile	
200 205 210	
gtt gtg gcg gaa ctt cgg gaa cgc cca gtt ggt act gcc gac cgt gaa	787
Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly Thr Ala Asp Arg Glu	
215 220 225	
aac tcc gtt ggt gtg gca ctt cgt gag ctt cgc cca cgc ctc atc ctg	835
Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg Pro Arg Leu Ile Leu	
230 235 240 245	
gat gca gaa cgc cgc aaa gtc tgc ctg cgt cta cct gaa cag cgc gtc	883
Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu Pro Glu Gln Arg Val	
250 255 260	
agc gac gat gaa atc aac tgg cga gtc agc cta gaa ggc acc acc cgg	931
Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu Glu Gly Thr Thr Arg	
265 270 275	
att ttc tcc acc cgc cga gca tgg ggc gat act tct gga tac tcc gaa	979
Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr Ser Gly Tyr Ser Glu	
280 285 290	
gcc ctc gac atc act gtc gag cgt caa atc cgc gaa acc acc gtc acc	1027
Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg Glu Thr Thr Val Thr	
295 300 305	
gac acc tca aac caa atc acc tgg gtt gtc cca gtc gtg gac ttc aac	1075
Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro Val Val Asp Phe Asn	
310 315 320 325	
gac cca gtg ctg gtg ttt tcc gcg cgc ggt gaa aac ctc acc gac aag	1123
Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu Asn Leu Thr Asp Lys	
330 335 340	
gtc tcc ctg cac cat caa gag att tac gtt ctc gcg cca gcg gaa gca	1171
Val Ser Leu His His Gln Glu Ile Tyr Val Leu Ala Pro Ala Glu Ala	
345 350 355	
aaa ctc gaa gac atg gtc act ggc cag cca gta cca gtt att gag caa	1219
Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln	
360 365 370	
ttc ctc gta gag ggc tgg aac tca tgg gtg tgc tcc cgc gtg gac gcc	1267
Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala	
375 380 385	
cgt ggc ctg tcc tct ctg aag gtc aac aaa gaa gtc cga tgc att gac	1315
Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu Val Arg Cys Ile Asp	
390 395 400 405	
cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac	1363
Pro Arg Arg Arg Val Ala Phe His His Pro Ala Glu Leu Val Pro His	
410 415 420	
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Val Arg Ser Ile Ser Gly Leu Pro Val His Ala Gln Ser Leu Ile Ala	
425 430 435	

gag ttc cca cca acc ctg agc gga caa gac gaa acc tgg atg ctc tcc	1459
Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser	
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Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly Glu Glu Ile Ala Glu	
455 460 465	
cca gag cct ttg gaa gtc cct gcc gac ggt ggc ctt ttc gcc atc ttc	1555
Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly Leu Phe Ala Ile Phe	
470 475 480 485	
gac cca gaa ata tac gac gcc cca tgg gtg ggt gaa tac ctg gtc cga	1603
Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly Glu Tyr Leu Val Arg	
490 495 500	
ctc cgc ggc cca cgc aat gaa tcc ttc cga ccc gaa ttc gcc atc gtc	1651
Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro Glu Phe Ala Ile Val	
505 510 515	
gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga	1699
Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg	
520 525 530	
atc cca acc acc act ggt ctc agc gaa gcc agc cta cgc gtg cgt tcc	1747
Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser Leu Arg Val Arg Ser	
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ggt gaa aag cac ttc acc gca gag cca cgc ctg gtc acc gtt gaa gca	1795
Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu Val Thr Val Glu Ala	
550 555 560 565	
acc gac ccc aac gca tca ttc gtg gtc acc acc gat gaa ggc gat caa	1843
Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr Asp Glu Gly Asp Gln	
570 575 580	
atg cca ttg cga ttt gtg cca cca caa atc gcc atc gaa ctt cca ctg	1891
Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala Ile Glu Leu Pro Leu	
585 590 595	
acc acc gag cca cca acc tgg cgc gtc acc cgt act gtc tgt gga cca	1939
Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg Thr Val Cys Gly Pro	
600 605 610	
cgc gac ctc gac ggt gca ggc gaa ctc cgc atc cgc acc ggt gtc gat	1987
Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile Arg Thr Gly Val Asp	
615 620 625	
gtc ggc gat cca aag gtc agt gtg cgc aac cac cac ggt tca cca ctg	2035
Val Gly Asp Pro Lys Val Ser Val Arg Asn His His Gly Ser Pro Leu	
630 635 640 645	
cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc	2083
Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala	
650 655 660	
agc atg aag gaa atc gca gcc agt acc ttt gtg atg cca cgc gga tcc	2131
Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val Met Pro Arg Gly Ser	
665 670 675	
atc gaa ttt gag tgg act gac cgc aag gtt gac cgt cgc gtt tcc gtg	2179

Ile	Glu	Phe	Glu	Trp	Thr	Asp	Arg	Lys	Val	Asp	Arg	Arg	Val	Ser	Val		
		680					685					690					
acg	att	gct	gtc	att	gac	aaa	act	gag	aac	ttt	act	ggc	atc	acc	atc	2227	
Thr	Ile	Ala	Val	Ile	Asp	Lys	Thr	Glu	Asn	Phe	Thr	Gly	Ile	Thr	Ile		
	695					700				705							
gaa	gat	gga	aag	ctc	gta	ttc	gaa	gaa	ctc	gca	gcc	ggt	cgc	caa	ctc	2275	
Glu	Asp	Gly	Lys	Leu	Val	Phe	Glu	Glu	Leu	Ala	Ala	Gly	Arg	Gln	Leu		
710					715					720					725		
gct	gca	tgg	gtg	tgg	cca	caa	acc	gca	ccg	tgg	gta	agc	gca	gtg	gaa	2323	
Ala	Ala	Trp	Val	Trp	Pro	Gln	Thr	Ala	Pro	Trp	Val	Ser	Ala	Val	Glu		
				730					735					740			
ctt	gct	gtc	acc	gga	cca	gag	ctg	gaa	ctc	cct	gaa	gtt	ctc	gtc	ggc	2371	
Leu	Ala	Val	Thr	Gly	Pro	Glu	Leu	Glu	Leu	Pro	Glu	Val	Leu	Val	Gly		
			745					750					755				
gca	ggc	aac	ctg	att	gtt	caa	ctc	cac	acc	gct	gac	cca	ttc	act	acc	2419	
Ala	Gly	Asn	Leu	Ile	Val	Gln	Leu	His	Thr	Ala	Asp	Pro	Phe	Thr	Thr		
		760					765					770					
tcc	gtg	acc	cca	ctg	tca	cca	gga	aaa	gct	gcg	gtc	acc	gtt	gag	caa	2467	
Ser	Val	Thr	Pro	Leu	Ser	Pro	Gly	Lys	Ala	Ala	Val	Thr	Val	Glu	Gln		
		775				780						785					
gaa	ggc	tac	tac	tca	gca	caa	acc	gaa	gaa	tat	gca	cag	ctt	tca	gca	2515	
Glu	Gly	Tyr	Tyr	Ser	Ala	Gln	Thr	Glu	Glu	Tyr	Ala	Gln	Leu	Ser	Ala		
790					795					800					805		
ttc	ttc	ggt	ggg	gaa	gta	gaa	gaa	cca	cca	atc	agt	gac	gct	gtg	gtc	2563	
Phe	Phe	Gly	Gly	Glu	Val	Glu	Glu	Pro	Pro	Ile	Ser	Asp	Ala	Val	Val		
				810					815					820			
ccc	gca	ctt	tgg	gat	gtt	tcc	cat	atc	tgg	acc	gaa	cag	gga	aac	acc	2611	
Pro	Ala	Leu	Trp	Asp	Val	Ser	His	Ile	Trp	Thr	Glu	Gln	Gly	Asn	Thr		
			825					830					835				
gag	cat	ctt	cca	gta	gtc	cat	gcc	gcc	ctg	cgc	tcc	tca	cca	gcc	gca	2659	
Glu	His	Leu	Pro	Val	Val	His	Ala	Ala	Leu	Arg	Ser	Ser	Pro	Ala	Ala		
		840					845					850					
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Ala	Leu	Lys	Gly	Leu	Ser	Ala	Ser	Leu	Val	Pro	Ala	Gln	Ala	Leu	Pro		
		855				860					865						
gga	aaa	gtc	att	tcc	tcc	gga	ctg	gca	gcc	tca	ccg	ttc	acc	acg	gaa	2755	
Gly	Lys	Val	Ile	Ser	Ser	Gly	Leu	Ala	Ala	Ser	Pro	Phe	Thr	Thr	Glu		
870					875					880					885		
tca	cca	gca	aca	gaa	gtg	cac	cgc	acc	gca	tgg	atc	gga	acc	ctg	caa	2803	
Ser	Pro	Ala	Thr	Glu	Val	His	Arg	Thr	Ala	Trp	Ile	Gly	Thr	Leu	Gln		
				890					895					900			
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Leu	Leu	Gly	Ala	Leu	Pro	Ser	Ala	Phe	Lys	Glu	Ala	Glu	Glu	Leu	Gly		
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aac	cgc	aca	cca	ctg	ctg	cca	atc	ctc	gga	caa	ctt	gag	gaa	gtc	gcc	2899	
Asn	Arg	Thr	Pro	Leu	Leu	Pro	Ile	Leu	Gly	Gln	Leu	Glu	Glu	Val	Ala		

920	925	930	
ggc aag aac atc ctg tcc acc ctt gca act ggc cgt gac tcc act ttg Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly Arg Asp Ser Thr Leu 935 940 945			2947
gac acc gca tgc atc gac caa tcc acc gtt gcg att gcc ggc atg aac Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala Ile Ala Gly Met Asn 950 955 960 965			2995
gaa acc cag caa aaa gcc ctg ctg gac atg ttc ttc agc aac gcc gac Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe Phe Ser Asn Ala Asp 970 975 980			3043
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gaa ggc ttg att aag acc gct gta gaa ctt ctt cgt gcc atg cgt gga Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu Arg Ala Met Arg Gly 1015 1020 1025			3187
acc cag cgt cag ctg tat tcc tcc gca cgt att cga ttc gac aag ctc Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile Arg Phe Asp Lys Leu 1030 1035 1040 1045			3235
gat ggt gtc aac act gac aac cca gaa aac atg tgg gca ctc acc cca Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met Trp Ala Leu Thr Pro 1050 1055 1060			3283
gtt gtg tca ctg gtg ttc gcg ttg tca tcc cgt ttg cat gca cac gaa Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg Leu His Ala His Glu 1065 1070 1075			3331
ttg atc ggc aag acc cga act ctc gat cgt gca tct gcc ggt tgg ggt Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala Ser Ala Gly Trp Gly 1080 1085 1090			3379
cga atc gct gat ctg gtg cca gac ctt gtc acc ggt gac ttg atc tcc Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr Gly Asp Leu Ile Ser 1095 1100 1105			3427
gcg gag gca atg gtt ttg gga gct cga aac cca gga ctc gtc gat Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro Gly Leu Val Asp 1110 1115 1120			3472
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<211> 1124

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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 20 25 30
 Phe Pro Gln Ile Gln Leu Arg His Asp Glu Leu Glu Arg Ile His Arg
 35 40 45
 Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
 50 55 60
 Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
 65 70 75 80
 Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr
 85 90 95
 Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly
 100 105 110
 Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly
 115 120 125
 Ile Ala Ser Pro Leu Glu Leu Leu Ser Ile His Ala Gly Ile Ser Asn
 130 135 140
 His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu
 145 150 155 160
 Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala
 165 170 175
 Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr
 180 185 190
 His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala
 195 200 205
 Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly
 210 215 220
 Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg
 225 230 235 240
 Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu
 245 250 255
 Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu
 260 265 270
 Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr
 275 280 285
 Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg
 290 295 300
 Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro
 305 310 315 320
 Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu
 325 330 335

Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu
 340 345 350
 Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val
 355 360 365
 Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys
 370 375 380
 Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu
 385 390 395 400
 Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala
 405 410 415
 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
 420 425 430
 Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu
 435 440 445
 Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly
 450 455 460
 Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly
 465 470 475 480
 Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
 485 490 495
 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
 500 505 510
 Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
 515 520 525
 Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
 530 535 540
 Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
 545 550 555 560
 Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
 565 570 575
 Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
 580 585 590
 Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
 595 600 605
 Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
 610 615 620
 Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
 625 630 635 640
 His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
 645 650 655
 Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val

660							665					670				
Met	Pro	Arg	Gly	Ser	Ile	Glu	Phe	Glu	Trp	Thr	Asp	Arg	Lys	Val	Asp	
		675					680					685				
Arg	Arg	Val	Ser	Val	Thr	Ile	Ala	Val	Ile	Asp	Lys	Thr	Glu	Asn	Phe	
		690					695					700				
Thr	Gly	Ile	Thr	Ile	Glu	Asp	Gly	Lys	Leu	Val	Phe	Glu	Glu	Leu	Ala	
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Ala	Gly	Arg	Gln	Leu	Ala	Ala	Trp	Val	Trp	Pro	Gln	Thr	Ala	Pro	Trp	
			725					730					735			
Val	Ser	Ala	Val	Glu	Leu	Ala	Val	Thr	Gly	Pro	Glu	Leu	Glu	Leu	Pro	
			740					745					750			
Glu	Val	Leu	Val	Gly	Ala	Gly	Asn	Leu	Ile	Val	Gln	Leu	His	Thr	Ala	
		755					760					765				
Asp	Pro	Phe	Thr	Thr	Ser	Val	Thr	Pro	Leu	Ser	Pro	Gly	Lys	Ala	Ala	
		770					775					780				
Val	Thr	Val	Glu	Gln	Glu	Gly	Tyr	Tyr	Ser	Ala	Gln	Thr	Glu	Glu	Tyr	
785							790					795				
Ala	Gln	Leu	Ser	Ala	Phe	Phe	Gly	Gly	Glu	Val	Glu	Glu	Pro	Pro	Ile	
			805					810					815			
Ser	Asp	Ala	Val	Val	Pro	Ala	Leu	Trp	Asp	Val	Ser	His	Ile	Trp	Thr	
			820					825					830			
Glu	Gln	Gly	Asn	Thr	Glu	His	Leu	Pro	Val	Val	His	Ala	Ala	Leu	Arg	
		835					840					845				
Ser	Ser	Pro	Ala	Ala	Ala	Leu	Lys	Gly	Leu	Ser	Ala	Ser	Leu	Val	Pro	
		850					855					860				
Ala	Gln	Ala	Leu	Pro	Gly	Lys	Val	Ile	Ser	Ser	Gly	Leu	Ala	Ala	Ser	
865							870					875				
Pro	Phe	Thr	Thr	Glu	Ser	Pro	Ala	Thr	Glu	Val	His	Arg	Thr	Ala	Trp	
			885					890					895			
Ile	Gly	Thr	Leu	Gln	Leu	Leu	Gly	Ala	Leu	Pro	Ser	Ala	Phe	Lys	Glu	
			900					905					910			
Ala	Glu	Glu	Leu	Gly	Asn	Arg	Thr	Pro	Leu	Leu	Pro	Ile	Leu	Gly	Gln	
		915					920					925				
Leu	Glu	Glu	Val	Ala	Gly	Lys	Asn	Ile	Leu	Ser	Thr	Leu	Ala	Thr	Gly	
		930					935					940				
Arg	Asp	Ser	Thr	Leu	Asp	Thr	Ala	Cys	Ile	Asp	Gln	Ser	Thr	Val	Ala	
		945					950					955				
Ile	Ala	Gly	Met	Asn	Glu	Thr	Gln	Gln	Lys	Ala	Leu	Leu	Asp	Met	Phe	
			965					970					975			
Phe	Ser	Asn	Ala	Asp	Ile	Val	Pro	Gly	Pro	Leu	Met	Glu	Asp	Asn	Thr	
		980					985					990				

Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg
 995 1000 1005
 Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
 1010 1015 1020
 Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
 1025 1030 1035 1040
 Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met
 1045 1050 1055
 Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg
 1060 1065 1070
 Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala
 1075 1080 1085
 Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr
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 Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro
 1105 1110 1115 1120
 Gly Leu Val Asp

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 <223> RXN02266

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 tgtaccggcc ttttattgat tttgacgtaa gcttgcaccg atg act caa gat gaa 115
 Met Thr Gln Asp Glu
 1 5
 cac ccc cga cag gcc gac tcc cat ttc aac atg ctt tta ccg gat gga 163
 His Pro Arg Gln Ala Asp Ser His Phe Asn Met Leu Leu Pro Asp Gly
 10 15 20
 aat gaa aac gca cac cag ctt tct gtc gct cta aat cag gtg gca cat 211
 Asn Glu Asn Ala His Gln Leu Ser Val Ala Leu Asn Gln Val Ala His
 25 30 35
 ctg ttg gcc tat gat gcg gac tct tca att cat cgg cct gat ggg cta 259
 Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His Arg Pro Asp Gly Leu
 40 45 50
 agt ctg gcg tcc tat aga att ctc ttt tca ctg tgg act gat ggc ccg 307
 Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu Trp Thr Asp Gly Pro
 55 60 65

atg agt cca ctc cag gtg act gac aag act gga atg aaa aag tct gcg 355
 Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly Met Lys Lys Ser Ala
 70 75 80 85
 att tct aac ctg tta aag cca ttg ctc gct gaa tct ctg att gtg cag 403
 Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu Ser Leu Ile Val Gln
 90 95 100
 gtg acg gca gaa aat gat cga cgc tca aag gtt tta agc ctt agc gaa 451
 Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val Leu Ser Leu Ser Glu
 105 110 115
 aaa ggc act aca tac att cag aaa aca gcc acc cgc caa aat gct ttg 499
 Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr Arg Gln Asn Ala Leu
 120 125 130
 gaa tcc gag tgg ttt ggc acc ctg acc gac atc gag cag gat tta ttg 547
 Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile Glu Gln Asp Leu Leu
 135 140 145
 gag tcg ttg ctc agg aaa ctg ctc gac tcc aac cgc gca tcc aag gtt 595
 Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn Arg Ala Ser Lys Val
 150 155 160 165
 cgt aaa aac cga tct aac tagcgctcgat ccttagggat gta 636
 Arg Lys Asn Arg Ser Asn
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 20 25 30
 Asn Gln Val Ala His Leu Leu Ala Tyr Asp Ala Asp Ser Ser Ile His
 35 40 45
 Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
 50 55 60
 Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
 65 70 75 80
 Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
 85 90 95
 Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
 100 105 110
 Leu Ser Leu Ser Glu Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr
 115 120 125
 Arg Gln Asn Ala Leu Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile

130	135	140
Glu Gln Asp Leu Leu Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn		
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Arg Ala Ser Lys Val Arg Lys Asn Arg Ser Asn		
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 <223> RXN02362

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 aattatttga tccgattctt ccgttcaaag gectcattcc gtg act atc tct cgc 115
 Val Thr Ile Ser Arg
 1 5
 cga ctc aaa caa gag cgc agt ttc gct gac gat ctt caa gat ctc aaa 163
 Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys
 10 15 20
 act ctc aat gat caa ctg cgg ttt aca aac gcc aaa ttg caa gct cgc 211
 Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala Lys Leu Gln Ala Arg
 25 30 35
 atc agt ggt att ggc aat gat gga aag aaa atc acg cgc cct acc cca 259
 Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile Thr Arg Pro Thr Pro
 40 45 50
 ctc ctt gcg ctg gat ttt cag ctg acc gtt gaa gaa tac gaa acg atc 307
 Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu Glu Tyr Glu Thr Ile
 55 60 65
 att gca atc ttg gtg gaa gca gtt ggc gga aat caa tcc aag cca gcg 355
 Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn Gln Ser Lys Pro Ala
 70 75 80 85
 att ctt aaa gat ctg ttt ata gaa tat cca ctc gtc ttc ctg gca gcg 403
 Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu Val Phe Leu Ala Ala
 90 95 100
 ctt tct gga acc gcc atg ctc gat gct caa gaa ggt ttc tgg cct gcg 451
 Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu Gly Phe Trp Pro Ala
 105 110 115
 ttc tgg aaa cgc act cag gtg tca gtt cca gag cat gta tac gac gcg 499
 Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu His Val Tyr Asp Ala
 120 125 130
 atc cgt aaa gaa cta gtt aat agc atc cgc aaa aat ggc cta gaa act 547
 Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys Asn Gly Leu Glu Thr
 135 140 145

ttt tct ctc gct gac ctc aat cga cgc gaa tat gtc gga ctc atc caa	595
Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr Val Gly Leu Ile Gln	
150 155 160 165	
ctt cac agt ggc ctt tct gca aaa gac atg ctc gcc ttg gtc aaa ttt	643
Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu Ala Leu Val Lys Phe	
170 175 180	
atc gat cac act cga gca gaa aac caa gga tgg gat tct ggt gag gac	691
Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp Asp Ser Gly Glu Asp	
185 190 195	
ttt gca tca tat gcg aag agt gtc ttc tcc tcc ggg gac aac cta tta	739
Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser Gly Asp Asn Leu Leu	
200 205 210	
acc acg gag tcg ctc aag caa tta gtc acc cac atc cct gcg cgt tcc	787
Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His Ile Pro Ala Arg Ser	
215 220 225	
gtc gac ttc atc gcc aga gtc tat gaa cta acc aat tgg tac cgc gac	835
Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr Asn Trp Tyr Arg Asp	
230 235 240 245	
ctc aaa gac ctc aat gaa gta gaa gcc ttc gta ggt act cat ggg ctg	883
Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val Gly Thr His Gly Leu	
250 255 260	
ccg gaa ttg tct ttc aaa ttt ctt ctg gag tgt ctg agc ggc gaa gct	931
Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys Leu Ser Gly Glu Ala	
265 270 275	
gaa caa att gcc gaa aag acg aaa gca gca cca gca agc ctg gaa aac	979
Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro Ala Ser Leu Glu Asn	
280 285 290	
ctg gaa cct ccg cat ctc tat ctg gat cca cag agt ttt gaa ctc agt	1027
Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln Ser Phe Glu Leu Ser	
295 300 305	
ctt gtt ttc cca gcg atc tct aaa act gca gca ctt cag att cca gca	1075
Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala Leu Gln Ile Pro Ala	
310 315 320 325	
cca gaa tgg aca gtg att tat gac gga aac tcc att aaa gtt cgt ccc	1123
Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser Ile Lys Val Arg Pro	
330 335 340	
gaa cag gac tgg tcc tac gga ggt ttc gcc gaa tac cgt ttg cct tta	1171
Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu Tyr Arg Leu Pro Leu	
345 350 355	
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Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr Pro Thr Glu Lys Ser	
360 365 370	
cta att ctg att gaa gga ttt ggc cac aag aat ccc att atg ttc ttt	1267
Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn Pro Ile Met Phe Phe	
375 380 385	

aag aac aac ggt cag cca tat gca aac caa gaa atg ctc agt ggc aac	1315
Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu Met Leu Ser Gly Asn	
390 395 400 405	
gct gtc aca gct ata gtc cca gct gca gca atc att cgt gca cgt atg	1363
Ala Val Thr Ala Ile Val Pro Ala Ala Ile Ile Arg Ala Arg Met	
410 415 420	
cga gct tcc aag act ttc aac tat caa gac ttg ggt ccc ttg tcc gga	1411
Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu Gly Pro Leu Ser Gly	
425 430 435	
tgg aac aag tgg gtc att cgt tgc atc cca ctc aaa cga gct gaa tcg	1459
Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu Lys Arg Ala Glu Ser	
440 445 450	
atc aca gtc tcc cac ggt ggc ttc aga aaa gaa ctc cca gtt cga cgc	1507
Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu Leu Pro Val Arg Arg	
455 460 465	
aaa gtt gat gtt caa tgg att act gag gat ctc acg atc gag aat ctt	1555
Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu Thr Ile Glu Asn Leu	
470 475 480 485	
caa ggt ctc gat cat gag ccc gtt ttc cac acg agt ccc cgc atc gaa	1603
Gln Gly Leu Asp His Glu Pro Val Phe His Thr Ser Pro Arg Ile Glu	
490 495 500	
ttc ccc acc tct gga tca aac tgg gta att cag tat tca cag att ctt	1651
Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln Tyr Ser Gln Ile Leu	
505 510 515	
cca gat ggc agc ctc atc gaa atg gaa gat tac cca gtc gaa cct gaa	1699
Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr Pro Val Glu Pro Glu	
520 525 530	
aac ttc gga tac gaa cta gac ctc ttc gaa gaa tcc gac gac cct tgg	1747
Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu Ser Asp Asp Pro Trp	
535 540 545	
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Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp Glu Lys Val Tyr Glu	
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Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp Leu Ser Leu Thr Phe	
570 575 580	
agc gga ggc gga cct gaa aat cga ttt agg tac ccc agc atc aat cag	1891
Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr Pro Ser Ile Asn Gln	
585 590 595	
gga caa act ggc tta aca aag act ttc gcc cgt ttt agt tcc aat tct	1939
Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg Phe Ser Ser Asn Ser	
600 605 610	
gaa aag cac atc agg ttc cca gat gag atc atc ggg ctt gat gca ttc	1987
Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile Gly Leu Asp Ala Phe	
615 620 625	
acc tct caa aaa gcg ttt aac atc gca agc ggt gat ttc cct gag gac	2035

Thr 630	Ser	Gln	Lys	Ala	Phe 635	Asn	Ile	Ala	Ser	Gly 640	Asp	Phe	Pro	Glu	Asp 645	
tac	aac	ctc	gac	gtt	ttc	atc	acg	cct	ccg	caa	ctt	cac	tac	caa	gta	2083
Tyr	Asn	Leu	Asp	Val	Phe 650	Ile	Thr	Pro	Pro	Gln	Leu	His	Tyr	Gln	Val	
cct	gtc	aca	cac	agc	caa	aca	aag	tgg	gaa	agc	aca	aag	acg	aca	cta	2131
Pro	Val	Thr	His	Ser	Gln	Thr	Lys	Trp	Glu	Ser	Thr	Lys	Thr	Thr	Leu	
gat	ttc	aat	gac	ttt	gcc	gat	gga	aac	ctc	cag	atc	aga	ttc	cct	aat	2179
Asp	Phe	Asn	Asp	Phe	Ala	Asp	Gly	Asn	Leu	Gln	Ile	Arg	Phe	Pro	Asn	
gaa	gtc	tat	gat	cca	aac	ttg	aaa	atc	att	aaa	atg	gtg	gca	tac	aag	2227
Glu	Val	Tyr	Asp	Pro	Asn	Leu	Lys	Ile	Ile	Lys	Met	Val	Ala	Tyr	Lys	
aaa	cct	gag	tcc	agt	gag	cct	aaa	tac	tta	agc	aaa	att	ggg	tca	agc	2275
Lys	Pro	Glu	Ser	Ser	Glu	Pro	Lys	Tyr	Leu	Ser	Lys	Ile	Gly	Ser	Ser	
aaa	gtg	tgg	tct	atc	cct	atg	gat	cgc	atc	aag	gaa	ctc	atg	gat	gat	2323
Lys	Val	Trp	Ser	Ile	Pro	Met	Asp	Arg	Ile	Lys	Glu	Leu	Met	Asp	Asp	
gat	gcc	caa	ttc	ctt	ttg	atc	gcg	gag	tgg	ttc	gct	gaa	agt	aaa	gac	2371
Asp	Ala	Gln	Phe	Leu	Leu	Ile	Ala	Glu	Trp	Phe	Ala	Glu	Ser	Lys	Asp	
cag	cac	cga	gag	aag	atc	att	agc	gaa	gct	aag	cga	act	gga	aaa	atc	2419
Gln	His	Arg	Glu	Lys	Ile	Ile	Ser	Glu	Ala	Lys	Arg	Thr	Gly	Lys	Ile	
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Ser	Asn	Ala	Ala	Leu	Lys	Ser	Ala	Arg	Pro	Gln	Pro	Gln	Ala	Ser	Ser	
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His	Ile	Ala	Thr	Ile	Glu	Lys	Lys	Pro	Leu	Leu	Ala	Ala	Ala	Glu	Ile	
aag	ctt	tct	acc	gtg	gag	ttg	gaa	ctt	ggg	cgg	cac	act	tct	aag	aga	2563
Lys	Leu	Ser	Thr	Val	Glu	Leu	Glu	Leu	Gly	Arg	His	Thr	Ser	Lys	Arg	
ctg	gaa	ggc	tgg	gca	tgg	tct	gcg	ctc	aac	ccg	ctt	gat	cca	cca	atc	2611
Leu	Glu	Gly	Trp	Ala	Trp	Ser	Ala	Leu	Asn	Pro	Leu	Asp	Pro	Pro	Ile	
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Lys	Val	Asp	Phe	Gln	Gly	Thr	Ser	Gly	Ser	Leu	Pro	Asp	Thr	His	Phe	
gtc	gtt	ggc	cct	tta	atc	gtg	gaa	gtg	aga	gaa	aaa	gag	ttt	ctc	tcc	2707
Val	Val	Gly	Pro	Leu	Ile	Val	Glu	Val	Arg	Glu	Lys	Glu	Phe	Leu	Ser	
caa	tgg	cag	cca	aaa	gtt	ccc	tca	gtt	aaa	gcc	gtg	gtt	gca	aat	gat	2755
Gln	Trp	Gln	Pro	Lys	Val	Pro	Ser	Val	Lys	Ala	Val	Val	Ala	Asn	Asp	

870	875	880	885	
ccc tca ttt gaa ttg gac cct caa ttt gat cct ttc ctc aca cac cga				2803
Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro Phe Leu Thr His Arg	890	895	900	
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Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu Leu Pro Gln Glu Ile	905	910	915	
cgc aca gtg tgg gac gcc cga ttc aat atg cgc cat gtc tta gcg cag				2899
Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg His Val Leu Ala Gln	920	925	930	
cgt gaa aac ctt cat gtg aaa tcg att caa gat ttt gac gat gcc acc				2947
Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp Phe Asp Asp Ala Thr	935	940	945	
agt acc tat ctc acc agt gat cct cgg gtg gca tta gat gaa ttg gat				2995
Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala Leu Asp Glu Leu Asp	950	955	960	965
aag agc tca att ccg tct aat tcc cac ttt gaa tca ttc atc cga tcc				3043
Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu Ser Phe Ile Arg Ser	970	975	980	
gga tta gct gag ctt tct ttc gaa gtt gac gac aca gcc gga gat atc				3091
Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp Thr Ala Gly Asp Ile	985	990	995	
cat cgc gtt ccc tgg atc ggc ctg atc cag gaa atg aac gac ctc aga				3139
His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu Met Asn Asp Leu Arg	1000	1005	1010	
att ctg cag ata caa ggc tat gaa aca gaa gaa cga gcc atc gaa cgc				3187
Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu Arg Ala Ile Glu Arg	1015	1020	1025	
cga aat tcg cag agc tac atc cgt gag ata gga ggc agt gaa ttg tgg				3235
Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly Gly Ser Glu Leu Trp	1030	1035	1040	1045
aat atc cta aaa gga aat tca gag gga ttg tct ctt gct caa aaa tgc				3283
Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser Leu Ala Gln Lys Cys	1050	1055	1060	
gca cca caa gcc act gag att aat gtg att cgt aat tca ggc ttg gaa				3331
Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg Asn Ser Gly Leu Glu	1065	1070	1075	
gct atg cgc aat ggg ctg ggc gcc gat cag ttc agc gcc gag ttt att				3379
Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe Ser Ala Glu Phe Ile	1080	1085	1090	
tca gca gac tca cgc cta cga gct cag ctt gaa tgg ttg gaa aac cgc				3427
Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu Trp Leu Glu Asn Arg	1095	1100	1105	
cga gag ctc aat gat ctc ggc cag ctc cca acg ctc ttc gat ttc gcc				3475
Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr Leu Phe Asp Phe Ala	1110	1115	1120	1125

gag aaa tac gag tac ctc atc gat cac tta ggt gat gat cgc atc aag 3523
 Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly Asp Asp Arg Ile Lys
 1130 1135 1140

gtc act gca cgt gag ctg tct act ctt gcg tcg gaa cac cgt cgc ggc 3571
 Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser Glu His Arg Arg Gly
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aac gct gaa aac tgg ctt tat gca cca tat gtg tca ttc att tac agc 3619
 Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val Ser Phe Ile Tyr Ser
 1160 1165 1170

ttg ctt aac cga atg atc gct cat gaa gta ata cgt ccg atc gct cag 3667
 Leu Leu Asn Arg Met Ile Ala His Glu Val Ile Arg Pro Ile Ala Gln
 1175 1180 1185

atc aat tac tca cgg cac gat tgg gca aac gct gct cgg ctg att cct 3715
 Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala Ala Arg Leu Ile Pro
 1190 1195 1200 1205

cgt ctc aca gga ttt gac ctg gtg agt gcc gaa gcg aaa gtg ctc agc 3763
 Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu Ala Lys Val Leu Ser
 1210 1215 1220

gca ata aac aac aac aat ata atc cca act gca att taaggatcac 3809
 Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala Ile
 1225 1230

tatgtccaac gca 3822

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<211> 1233

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

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Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
 35 40 45

Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
 50 55 60

Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
 65 70 75 80

Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
 85 90 95

Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
 100 105 110

Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
 115 120 125

His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
 130 135 140
 Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
 145 150 155 160
 Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
 165 170 175
 Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
 180 185 190
 Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
 195 200 205
 Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
 210 215 220
 Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
 225 230 235 240
 Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
 245 250 255
 Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
 260 265 270
 Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
 275 280 285
 Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
 290 295 300
 Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
 305 310 315 320
 Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
 325 330 335
 Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
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 355 360 365
 Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
 370 375 380
 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
 385 390 395 400
 Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
 405 410 415
 Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
 420 425 430
 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
 435 440 445

Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
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 Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
 465 470 475 480
 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
 485 490 495
 Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
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 Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
 515 520 525
 Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
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 545 550 555 560
 Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
 565 570 575
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 580 585 590
 Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
 595 600 605
 Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
 610 615 620
 Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
 625 630 635 640
 Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
 645 650 655
 Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
 660 665 670
 Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
 675 680 685
 Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
 690 695 700
 Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
 705 710 715 720
 Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
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 Glu Leu Met Asp Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
 740 745 750
 Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
 755 760 765
 Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln

770					775					780					
Pro	Gln	Ala	Ser	Ser	His	Ile	Ala	Thr	Ile	Glu	Lys	Lys	Pro	Leu	Leu
785					790					795					800
Ala	Ala	Ala	Glu	Ile	Lys	Leu	Ser	Thr	Val	Glu	Leu	Glu	Leu	Gly	Arg
				805					810					815	
His	Thr	Ser	Lys	Arg	Leu	Glu	Gly	Trp	Ala	Trp	Ser	Ala	Leu	Asn	Pro
			820					825					830		
Leu	Asp	Pro	Pro	Ile	Lys	Val	Asp	Phe	Gln	Gly	Thr	Ser	Gly	Ser	Leu
		835					840					845			
Pro	Asp	Thr	His	Phe	Val	Val	Gly	Pro	Leu	Ile	Val	Glu	Val	Arg	Glu
		850					855					860			
Lys	Glu	Phe	Leu	Ser	Gln	Trp	Gln	Pro	Lys	Val	Pro	Ser	Val	Lys	Ala
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Val	Val	Ala	Asn	Asp	Pro	Ser	Phe	Glu	Leu	Asp	Pro	Gln	Phe	Asp	Pro
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			900					905					910		
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His	Val	Leu	Ala	Gln	Arg	Glu	Asn	Leu	His	Val	Lys	Ser	Ile	Gln	Asp
		930					935					940			
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945							950					955			960
Leu	Asp	Glu	Leu	Asp	Lys	Ser	Ser	Ile	Pro	Ser	Asn	Ser	His	Phe	Glu
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Ser	Phe	Ile	Arg	Ser	Gly	Leu	Ala	Glu	Leu	Ser	Phe	Glu	Val	Asp	Asp
			980					985					990		
Thr	Ala	Gly	Asp	Ile	His	Arg	Val	Pro	Trp	Ile	Gly	Leu	Ile	Gln	Glu
		995					1000					1005			
Met	Asn	Asp	Leu	Arg	Ile	Leu	Gln	Ile	Gln	Gly	Tyr	Glu	Thr	Glu	Glu
		1010					1015					1020			
Arg	Ala	Ile	Glu	Arg	Arg	Asn	Ser	Gln	Ser	Tyr	Ile	Arg	Glu	Ile	Gly
1025							1030					1035			1040
Gly	Ser	Glu	Leu	Trp	Asn	Ile	Leu	Lys	Gly	Asn	Ser	Glu	Gly	Leu	Ser
				1045					1050					1055	
Leu	Ala	Gln	Lys	Cys	Ala	Pro	Gln	Ala	Thr	Glu	Ile	Asn	Val	Ile	Arg
			1060					1065					1070		
Asn	Ser	Gly	Leu	Glu	Ala	Met	Arg	Asn	Gly	Leu	Gly	Ala	Asp	Gln	Phe
		1075					1080					1085			
Ser	Ala	Glu	Phe	Ile	Ser	Ala	Asp	Ser	Arg	Leu	Arg	Ala	Gln	Leu	Glu
		1090					1095					1100			

Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr
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Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
 1125 1130 1135

Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
 1140 1145 1150

Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
 1155 1160 1165

Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
 1170 1175 1180

Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
 1185 1190 1195 1200

Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
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Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Asn Ile Ile Pro Thr Ala
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<223> RXN02506

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 Met His Leu Asn Gln
 1 5

ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc 163
 Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala
 10 15 20

gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc 211
 Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser
 25 30 35

gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc 259
 Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe Glu Arg His Ser Arg
 40 45 50

ggg gtc tcc ctc aca aag gcc gga gaa atc ctc cac gaa gaa gcc ctc 307
 Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu His Glu Glu Ala Leu
 55 60 65

cga acg ctt agc agg atg caa tcg gta gtc gat gaa atc caa tcc ggt	355
Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp Glu Ile Gln Ser Gly	
70 75 80 85	
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Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val Pro Pro Gly Ile Pro	
90 95 100	
atc gac tgg ttg cgc tgc caa ctc atc gat tta ggc ccc gag acc cgc	451
Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu Gly Pro Glu Thr Arg	
105 110 115	
att tca ctg atc gaa tcc ccc acc gat gat cag cta aaa ctt ctt aaa	499
Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln Leu Lys Leu Leu Lys	
120 125 130	
caa cgc gaa ctc gac atc gcc ctt tgt cga cgc caa agc gag gcc ttt	547
Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg Gln Ser Glu Ala Phe	
135 140 145	
gcc acc aca ctt gtc cac gaa caa gaa ctg gga atc gtc gtc cga aaa	595
Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly Ile Val Val Arg Lys	
150 155 160 165	
aac tcc gaa ctg cac caa aaa gtc gca gga aaa gac aac gcc aca ctc	643
Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys Asp Asn Ala Thr Leu	
170 175 180	
ttc gat ctt gaa ggg ctt cga gtc ctc gca cac tcc cgc ggt gaa gta	691
Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His Ser Arg Gly Glu Val	
185 190 195	
aga att cag gaa gaa atc ctc aaa aac gcc atg ctc gcc gca gga gtt	739
Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met Leu Ala Ala Gly Val	
200 205 210	
aat gcc acg tgg atc ttc cga aaa ttt ggg caa tat agc tca ctg atc	787
Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln Tyr Ser Ser Leu Ile	
215 220 225	
gca gac ctt gtc cag gcc gat gtc gca ctc aca aca gag gaa tcc gcc	835
Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr Thr Glu Glu Ser Ala	
230 235 240 245	
cgc acc aac ttc ccc agc tgg caa tgg gtc ccc atc gaa ggc gaa gac	883
Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro Ile Glu Gly Glu Asp	
250 255 260	
gcc tcc gga aat gac ctt gtt gtt cgc acc tgg atc acc tgg aac ccc	931
Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp Ile Thr Trp Asn Pro	
265 270 275	
caa ccc acc ccc gcg gtg aag gcc ctg atc cag aaa ttt att gac gga	979
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 <212> PRT
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 Ser Arg Gln Ile Ser Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe
 35 40 45
 Glu Arg His Ser Arg Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu
 50 55 60
 His Glu Glu Ala Leu Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp
 65 70 75 80
 Glu Ile Gln Ser Gly Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val
 85 90 95
 Pro Pro Gly Ile Pro Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu
 100 105 110
 Gly Pro Glu Thr Arg Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln
 115 120 125
 Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
 130 135 140
 Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
 145 150 155 160
 Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
 165 170 175
 Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
 180 185 190
 Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
 195 200 205
 Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
 210 215 220
 Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
 225 230 235 240
 Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
 245 250 255
 Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
 260 265 270
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Lys Phe Ile Asp Gly Asn
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(766)

<223> RXN02620

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                                         Met Ala Gly Ala Val
                                         1                               5

gga cgc ccc cgg aga tca gct ccg cga cgg gca ggc aag aat cct cgc 163
Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg
                               10                               15                               20

gag gag att ctt gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc 211
Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe
                               25                               30                               35

gca aca acc tcc acg cat caa atc gct gat gcc gtg gga atc cgc caa 259
Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln
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gcc tcg ctg tat tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc 307
Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr
                               55                               60                               65

ctg ctg aaa tct act gtc gag ccg tcc act gtg ctc gcc gaa gac tta 355
Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu
                               70                               75                               80                               85

agc acc ctg gac gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc 403
Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala
                               90                               95                               100

tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg 451
Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu
                               105                               110                               115

tac caa ctc ccc atc gtt ggt tct gaa gag ttc gcc gag tac cac agc 499
Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser
                               120                               125                               130

cag cgc gaa gcc ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc 547
Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile
                               135                               140                               145

gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg 595
Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser
                               150                               155                               160                               165

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gca gac agc ctc ccg gag acc gca att atg ctt gcc gac gcc tcc ctc 691
 Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu
 185 190 195

gcc gtc ctc ggc gcg ccg ctg ccc gcc gac cgg gtc gaa aaa acg ctt 739
 Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu
 200 205 210

gaa cta atc aag cag gct gac gcg aaa taaccatccg cgccctgcgaa atc 789
 Glu Leu Ile Lys Gln Ala Asp Ala Lys
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Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala
 35 40 45

Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr
 50 55 60

Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val
 65 70 75 80

Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu
 85 90 95

Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp
 100 105 110

Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe
 115 120 125

Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp
 130 135 140

Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe
 145 150 155 160

His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile
 165 170 175

Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu
 180 185 190

Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg
 195 200 205

Val Glu Lys Thr Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
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<210> 293
 <211> 654
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(631)
 <223> RXN00826

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 Met Ile Thr Val Leu
 1 5
 att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta 163
 Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Leu Ala Gly Glu Leu
 10 15 20
 gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct 211
 Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
 25 30 35
 ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt 259
 Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
 40 45 50
 ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat 307
 Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
 55 60 65
 tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355
 Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
 70 75 80 85
 gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg 403
 Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
 90 95 100
 ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451
 Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
 105 110 115
 aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499
 Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
 120 125 130
 gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg 547
 Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
 135 140 145
 gat cat gag att gtg cta ggt tct gat gag gct tcg gga cga ccc gaa 595
 Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
 150 155 160 165

gaa atc tat gac agc ctg gga acg gcc cag agt tct taagaaagtt 641
Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser Ser
170 175

tgactagaga aca 654

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Asp Asp Phe Tyr Pro Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile
35 40 45
Val Ala Arg His Val Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp
50 55 60
Asp Trp His Asn Asn Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly
65 70 75 80
Arg Ser Leu Ile Ile Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys
85 90 95
Arg Lys Ala Ser Leu Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly
100 105 110
Pro Glu Ala Leu Arg Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr
115 120 125
Ala Pro Phe Trp Lys Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser
130 135 140
Leu Gly Val Glu Val Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala
145 150 155 160
Ser Gly Arg Pro Glu Glu Ile Tyr Asp Ser Leu Gly Thr Ala Gln Ser
165 170 175
Ser

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(532)
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 Val Gly Ile Asn Arg
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atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag 163
 Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln
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cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc 211
 Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser
 25 30 35

gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc 259
 Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly
 40 45 50

ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca 307
 Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala
 55 60 65

gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc 355
 Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys
 70 75 80 85

cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc 403
 His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg
 90 95 100

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att 451
 Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile
 105 110 115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt 499
 Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe
 120 125 130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552
 Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
 135 140

ctg 555

<210> 296

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val
 1 5 10 15

Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile
 20 25 30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg
 35 40 45

Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu
 50 55 60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr
 65 70 75 80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys
 85 90 95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr
 100 105 110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His
 115 120 125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
 130 135 140

<210> 297
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(913)
 <223> RXS00133

<400> 297
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aatttgaagg tggataccca gcggattaa gatgatgaag atg cta ttc gtt cgg 115
 Met Leu Phe Val Arg
 1 5

cgg ctg aca tcg ctg aaa acc gca aca ggc atc cca gtc acc atg ttc 163
 Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe
 10 15 20

gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg 211
 Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly
 25 30 35

ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc 259
 Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly
 40 45 50

gtt ggt gga cgc gtc gtc gca acc cgt cgt ccg gtt ggt gtg agt gat 307
 Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro Val Gly Val Ser Asp
 55 60 65

tac acc agg gca aat gtc att tca cat gag aag gat tcc gcg att cag 355
 Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys Asp Ser Ala Ile Gln
 70 75 80 85

gat gag ggc ctt cat tcc att gtc gca gtt ccc gtg atc gtg cac cgc 403
 Asp Glu Gly Leu His Ser Ile Val Ala Val Pro Val Ile Val His Arg
 90 95 100

gaa att cgt ggc gtt ttg tat gtt ggc gtt cac tct gcg gtg cgt ctc 451

Glu Ile Arg Gly Val Leu Tyr Val Gly Val His Ser Ala Val Arg Leu
 105 110 115
 ggc gac act gtt att gaa gaa gtc acc atg act gcg cgc acg ttg gaa 499
 Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr Ala Arg Thr Leu Glu
 120 125 130
 caa aac ctg gcg atc aac tcc gcg ctt cgc cgc aat ggc gtt cct gat 547
 Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg Asn Gly Val Pro Asp
 135 140 145
 ggt cgc ggt tcc ctc aaa gct aac cgc gtg atg aat ggg gcg gag tgg 595
 Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met Asn Gly Ala Glu Trp
 150 155 160 165
 gag cag gtt cgt tcc act cat tcc aag ctg cgc atg ctg gca aat cgt 643
 Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg Met Leu Ala Asn Arg
 170 175 180
 gtg acc gat gag gat ctg cgc cgc gat ttg gaa gag ctt tgc gat cag 691
 Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu Glu Leu Cys Asp Gln
 185 190 195
 atg gtc acc cca gtc cgc atc aag cag acc acc aag ctg tcc gcg cgt 739
 Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr Lys Leu Ser Ala Arg
 200 205 210
 gag ttg gac gtg ctg gct tgt gtc gcg ctc ggt cac acc aac gtc gaa 787
 Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly His Thr Asn Val Glu
 215 220 225
 gct gct gaa gag atg ggc atc ggc gcg gaa acc gtc aag agc tac ctg 835
 Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr Val Lys Ser Tyr Leu
 230 235 240 245
 cgc tcg gtc atg cgc aag ctc ggc gcc cac acg cgc tac gag gca gtc 883
 Arg Ser Val Met Arg Lys Leu Gly Ala His Thr Arg Tyr Glu Ala Val
 250 255 260
 aac gca gca cgc cgg atc ggc gca ctg cct taaaaagatt ttgctttacg acg 936
 Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
 265 270

<210> 298

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

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 Pro Val Thr Met Phe Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile
 20 25 30
 Thr Gln Trp Val Gly Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile
 35 40 45
 Glu Pro Gly Val Gly Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro
 50 55 60

Val Gly Val Ser Asp Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys
 65 70 75 80
 Asp Ser Ala Ile Gln Asp Glu Gly Leu His Ser Ile Val Ala Val Pro
 85 90 95
 Val Ile Val His Arg Glu Ile Arg Gly Val Leu Tyr Val Gly Val His
 100 105 110
 Ser Ala Val Arg Leu Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr
 115 120 125
 Ala Arg Thr Leu Glu Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg
 130 135 140
 Asn Gly Val Pro Asp Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met
 145 150 155 160
 Asn Gly Ala Glu Trp Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg
 165 170 175
 Met Leu Ala Asn Arg Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu
 180 185 190
 Glu Leu Cys Asp Gln Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr
 195 200 205
 Lys Leu Ser Ala Arg Glu Leu Asp Val Leu Ala Cys Val Ala Leu Gly
 210 215 220
 His Thr Asn Val Glu Ala Ala Glu Glu Met Gly Ile Gly Ala Glu Thr
 225 230 235 240
 Val Lys Ser Tyr Leu Arg Ser Val Met Arg Lys Leu Gly Ala His Thr
 245 250 255
 Arg Tyr Glu Ala Val Asn Ala Ala Arg Arg Ile Gly Ala Leu Pro
 260 265 270

<210> 299

<211> 699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(676)

<223> RXS00144

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 ctttaacgga ccgcacagag aggcgggggaa ggaggtcacg atg agc gaa cgt aat 115
 Met Ser Glu Arg Asn
 1 5

 agt gct gta cta gaa ctc ctt aat gag gac gac gtc agc cgt acc atc 163
 Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp Val Ser Arg Thr Ile
 10 15 20

gca cgc atc gcg cac cag att att gag aaa acc gcg ctt gat tcc aaa 211
 Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr Ala Leu Asp Ser Lys
 25 30 35

gac gcg gat cgg gtc atg ttg tta ggt att ccc tca ggt gga gtc cca 259
 Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro Ser Gly Gly Val Pro
 40 45 50

ttg gcc cgt agg ctc gct gaa aag atc gaa gaa ttt tcc ggc gtt tcg 307
 Leu Ala Arg Arg Leu Ala Glu Lys Ile Glu Glu Phe Ser Gly Val Ser
 55 60 65

gta gat acc ggc gct gtt gat atc acc ttg tac agg gat gat ctt cga 355
 Val Asp Thr Gly Ala Val Asp Ile Thr Leu Tyr Arg Asp Asp Leu Arg
 70 75 80 85

aac aaa cca cac cgc gca ctg cag ccc acc tct att cca gca ggt ggt 403
 Asn Lys Pro His Arg Ala Leu Gln Pro Thr Ser Ile Pro Ala Gly Gly
 90 95 100

atc gat aac acc acc gtg att ttg gtg gat gat gtg ctg ttt tcc ggt 451
 Ile Asp Asn Thr Thr Val Ile Leu Val Asp Asp Val Leu Phe Ser Gly
 105 110 115

cgt acc atc cgc gct gca ctt gat gct ttg cgc gac gtt gga cgc ccc 499
 Arg Thr Ile Arg Ala Ala Leu Asp Ala Leu Arg Asp Val Gly Arg Pro
 120 125 130

aac tac atc cag tta gct gtg ttg gtt gac cgc ggt cat cgc cag ctg 547
 Asn Tyr Ile Gln Leu Ala Val Leu Val Asp Arg Gly His Arg Gln Leu
 135 140 145

ccc att cgc gct gac tat gtg ggc aaa aat ctc ccc acc gca cgc gcg 595
 Pro Ile Arg Ala Asp Tyr Val Gly Lys Asn Leu Pro Thr Ala Arg Ala
 150 155 160 165

gaa gac gtt tcc gtc atg ctt aca gaa atc gac ggc cgc gat gca gtc 643
 Glu Asp Val Ser Val Met Leu Thr Glu Ile Asp Gly Arg Asp Ala Val
 170 175 180

acg ctc acc cga gaa gac tct gaa ggg gat tcc tagatgaagc acctcctatc 696
 Thr Leu Thr Arg Glu Asp Ser Glu Gly Asp Ser
 185 190

cat 699

<210> 300

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Ser Glu Arg Asn Ser Ala Val Leu Glu Leu Leu Asn Glu Asp Asp
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Val Ser Arg Thr Ile Ala Arg Ile Ala His Gln Ile Ile Glu Lys Thr
 20 25 30

Ala Leu Asp Ser Lys Asp Ala Asp Arg Val Met Leu Leu Gly Ile Pro

35					40					45					
Ser	Gly	Gly	Val	Pro	Leu	Ala	Arg	Arg	Leu	Ala	Glu	Lys	Ile	Glu	Glu
50						55					60				
Phe	Ser	Gly	Val	Ser	Val	Asp	Thr	Gly	Ala	Val	Asp	Ile	Thr	Leu	Tyr
65					70					75					80
Arg	Asp	Asp	Leu	Arg	Asn	Lys	Pro	His	Arg	Ala	Leu	Gln	Pro	Thr	Ser
				85					90					95	
Ile	Pro	Ala	Gly	Gly	Ile	Asp	Asn	Thr	Thr	Val	Ile	Leu	Val	Asp	Asp
			100					105					110		
Val	Leu	Phe	Ser	Gly	Arg	Thr	Ile	Arg	Ala	Ala	Leu	Asp	Ala	Leu	Arg
	115						120					125			
Asp	Val	Gly	Arg	Pro	Asn	Tyr	Ile	Gln	Leu	Ala	Val	Leu	Val	Asp	Arg
	130					135					140				
Gly	His	Arg	Gln	Leu	Pro	Ile	Arg	Ala	Asp	Tyr	Val	Gly	Lys	Asn	Leu
145					150				155						160
Pro	Thr	Ala	Arg	Ala	Glu	Asp	Val	Ser	Val	Met	Leu	Thr	Glu	Ile	Asp
				165					170					175	
Gly	Arg	Asp	Ala	Val	Thr	Leu	Thr	Arg	Glu	Asp	Ser	Glu	Gly	Asp	Ser
			180					185					190		

<210> 301

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1207)

<223> RXS00205

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atccccacaat	aggggtacct	tccagaaagt	tggtgaggag	atg	gct	tcc	gaa	acc	115
				Met	Ala	Ser	Glu	Thr	
				1				5	

tcc	agc	ccg	aag	aag	cgg	gcc	acc	acg	ctc	aaa	gac	atc	gcg	caa	gca	163
Ser	Ser	Pro	Lys	Lys	Arg	Ala	Thr	Thr	Leu	Lys	Asp	Ile	Ala	Gln	Ala	
			10						15					20		

aca	cag	ctt	tca	gtc	agc	acg	gtg	tcc	cgg	gca	ttg	gcc	aac	aac	gcg	211
Thr	Gln	Leu	Ser	Val	Ser	Thr	Val	Ser	Arg	Ala	Leu	Ala	Asn	Asn	Ala	
			25					30					35			

agc	att	ccg	gaa	tcc	aca	cgc	atc	cga	gtg	gtt	gaa	gcc	gct	caa	aag	259
Ser	Ile	Pro	Glu	Ser	Thr	Arg	Ile	Arg	Val	Val	Glu	Ala	Ala	Gln	Lys	
		40					45					50				

ctg	aac	tac	cgt	ccc	aat	gcc	caa	gct	cgt	gca	ttg	cgg	aag	tcg	agg	307
Leu	Asn	Tyr	Arg	Pro	Asn	Ala	Gln	Ala	Arg	Ala	Leu	Arg	Lys	Ser	Arg	

55					60					65						
aca	gac	acc	atc	ggt	gtc	atc	att	cca	aac	att	gag	aac	cca	tat	ttc	355
Thr	Asp	Thr	Ile	Gly	Val	Ile	Ile	Pro	Asn	Ile	Glu	Asn	Pro	Tyr	Phe	
70					75					80					85	
tcc	tca	cta	gca	gca	tcg	att	caa	aaa	gct	gct	cgt	gaa	gct	ggg	gtg	403
Ser	Ser	Leu	Ala	Ala	Ser	Ile	Gln	Lys	Ala	Ala	Arg	Glu	Ala	Gly	Val	
				90					95					100		
tcc	acc	att	ttg	tcc	aac	tct	gaa	gaa	aac	cca	gag	ctg	ctt	ggt	cag	451
Ser	Thr	Ile	Leu	Ser	Asn	Ser	Glu	Glu	Asn	Pro	Glu	Leu	Leu	Gly	Gln	
			105					110					115			
act	ttg	gcg	atc	atg	gat	gac	caa	cgc	ctc	gat	gga	atc	atc	gtg	gtg	499
Thr	Leu	Ala	Ile	Met	Asp	Asp	Gln	Arg	Leu	Asp	Gly	Ile	Ile	Val	Val	
			120				125						130			
cca	cac	att	cag	tca	gag	gaa	caa	gtc	act	gac	ttg	gtt	aac	agg	gga	547
Pro	His	Ile	Gln	Ser	Glu	Glu	Gln	Val	Thr	Asp	Leu	Val	Asn	Arg	Gly	
			135				140					145				
gtg	cca	gta	gtg	ctg	gca	gac	cgt	agt	ttt	gtt	aac	tcg	tct	att	cct	595
Val	Pro	Val	Val	Leu	Ala	Asp	Arg	Ser	Phe	Val	Asn	Ser	Ser	Ile	Pro	
150					155					160					165	
tcg	gtt	acc	tca	gat	cca	gtt	cgc	ggc	atg	act	gaa	gct	gtg	gac	tta	643
Ser	Val	Thr	Ser	Asp	Pro	Val	Pro	Gly	Met	Thr	Glu	Ala	Val	Asp	Leu	
				170					175					180		
ctc	ctg	gca	gct	gac	gtg	caa	ttg	ggc	tac	ctt	gcc	ggc	ccg	cag	gat	691
Leu	Leu	Ala	Ala	Asp	Val	Gln	Leu	Gly	Tyr	Leu	Ala	Gly	Pro	Gln	Asp	
			185					190					195			
act	tcc	act	ggt	cag	ctg	cgt	ctt	aac	act	ttt	gaa	aga	cta	tgc	gtg	739
Thr	Ser	Thr	Gly	Gln	Leu	Arg	Leu	Asn	Thr	Phe	Glu	Arg	Leu	Cys	Val	
			200				205					210				
gac	cgc	ggc	atc	gtc	gga	gca	tct	gtc	tat	tac	ggt	ggc	tac	cgc	caa	787
Asp	Arg	Gly	Ile	Val	Gly	Ala	Ser	Val	Tyr	Tyr	Gly	Gly	Tyr	Arg	Gln	
			215			220					225					
gaa	tct	gga	tat	gac	ggc	atc	aag	gtg	ctg	atc	aag	cag	gga	gcc	aat	835
Glu	Ser	Gly	Tyr	Asp	Gly	Ile	Lys	Val	Leu	Ile	Lys	Gln	Gly	Ala	Asn	
230					235					240					245	
gcg	att	atc	gct	ggt	gac	tcc	atg	atg	acc	atc	ggt	gcg	ttg	ttg	gct	883
Ala	Ile	Ile	Ala	Gly	Asp	Ser	Met	Met	Thr	Ile	Gly	Ala	Leu	Leu	Ala	
				250					255					260		
ctt	cat	gag	atg	aat	ttg	aag	atc	ggt	gag	gat	gtg	cag	ctc	att	ggg	931
Leu	His	Glu	Met	Asn	Leu	Lys	Ile	Gly	Glu	Asp	Val	Gln	Leu	Ile	Gly	
			265					270					275			
ttt	gat	aac	aac	cca	att	ttc	cgg	ctg	cag	aat	cca	ccg	ctg	agc	atc	979
Phe	Asp	Asn	Asn	Pro	Ile	Phe	Arg	Leu	Gln	Asn	Pro	Pro	Leu	Ser	Ile	
			280				285					290				
att	gac	cag	cac	gta	caa	gag	atc	ggt	aag	cgt	gcg	ttt	gag	att	ctg	1027
Ile	Asp	Gln	His	Val	Gln	Glu	Ile	Gly	Lys	Arg	Ala	Phe	Glu	Ile	Leu	
			295			300					305					

cag aag ctg atc aat ggg gac acc gcg caa aaa tct gtg gtg att cca 1075
 Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys Ser Val Val Ile Pro
 310 315 320 325

acg cag ctc agc atc aat gga tca acg gcg gtt tcc caa aag gcg gcc 1123
 Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val Ser Gln Lys Ala Ala
 330 335 340

gca aag gca gca aaa gca gcc caa aaa gca gcc gcg aaa gcc gca cag 1171
 Ala Lys Ala Ala Lys Ala Ala Gln Lys Ala Ala Ala Lys Ala Ala Gln
 345 350 355

aac acg caa cac gag gtg agc cta gat ggt gaa ctc tgaacaagcg 1217
 Asn Thr Gln His Glu Val Ser Leu Asp Gly Glu Leu
 360 365

cttcacgcgc atg 1230

<210> 302

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Ala Ser Glu Thr Ser Ser Pro Lys Lys Arg Ala Thr Thr Leu Lys
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Asp Ile Ala Gln Ala Thr Gln Leu Ser Val Ser Thr Val Ser Arg Ala
 20 25 30

Leu Ala Asn Asn Ala Ser Ile Pro Glu Ser Thr Arg Ile Arg Val Val
 35 40 45

Glu Ala Ala Gln Lys Leu Asn Tyr Arg Pro Asn Ala Gln Ala Arg Ala
 50 55 60

Leu Arg Lys Ser Arg Thr Asp Thr Ile Gly Val Ile Ile Pro Asn Ile
 65 70 75 80

Glu Asn Pro Tyr Phe Ser Ser Leu Ala Ala Ser Ile Gln Lys Ala Ala
 85 90 95

Arg Glu Ala Gly Val Ser Thr Ile Leu Ser Asn Ser Glu Glu Asn Pro
 100 105 110

Glu Leu Leu Gly Gln Thr Leu Ala Ile Met Asp Asp Gln Arg Leu Asp
 115 120 125

Gly Ile Ile Val Val Pro His Ile Gln Ser Glu Glu Gln Val Thr Asp
 130 135 140

Leu Val Asn Arg Gly Val Pro Val Val Leu Ala Asp Arg Ser Phe Val
 145 150 155 160

Asn Ser Ser Ile Pro Ser Val Thr Ser Asp Pro Val Pro Gly Met Thr
 165 170 175

Glu Ala Val Asp Leu Leu Leu Ala Ala Asp Val Gln Leu Gly Tyr Leu
 180 185 190

Ala Gly Pro Gln Asp Thr Ser Thr Gly Gln Leu Arg Leu Asn Thr Phe
 195 200 205

Glu Arg Leu Cys Val Asp Arg Gly Ile Val Gly Ala Ser Val Tyr Tyr
 210 215 220

Gly Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile
 225 230 235 240

Lys Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile
 245 250 255

Gly Ala Leu Leu Ala Leu His Glu Met Asn Leu Lys Ile Gly Glu Asp
 260 265 270

Val Gln Leu Ile Gly Phe Asp Asn Asn Pro Ile Phe Arg Leu Gln Asn
 275 280 285

Pro Pro Leu Ser Ile Ile Asp Gln His Val Gln Glu Ile Gly Lys Arg
 290 295 300

Ala Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys
 305 310 315 320

Ser Val Val Ile Pro Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val
 325 330 335

Ser Gln Lys Ala Ala Ala Lys Ala Ala Lys Ala Ala Gln Lys Ala Ala
 340 345 350

Ala Lys Ala Ala Gln Asn Thr Gln His Glu Val Ser Leu Asp Gly Glu
 355 360 365

Leu

<210> 303
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXS00470

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ctcatagact ctattgtgga gtgttgaggc tgataagtga atg ggg gaa agc cct 115
 Met Gly Glu Ser Pro
 1 5

gaa aag gtg gcg ttc agg gtc ttc cct gat ggt ttg gtg tcg cag ggg 163
 Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly Leu Val Ser Gln Gly
 10 15 20

cat gac atg atc gaa gat atg agt aac aca cct gcg cct tat acc ccg 211
 His Asp Met Ile Glu Asp Met Ser Asn Thr Pro Ala Pro Tyr Thr Pro

25										30					35					
cag	cct	gcg	ggg	caa	gcg	gtg	cct	tta	tat	ccc	acg	ttt	acc	cgg	tca	259				
Gln	Pro	Ala	Gly	Gln	Ala	Val	Pro	Leu	Tyr	Pro	Thr	Phe	Thr	Arg	Ser					
		40					45					50								
aga	gat	ggt	cgg	gtt	gtt	gcg	ggt	gtc	gca	tcg	ggg	ctg	gca	aag	cat	307				
Arg	Asp	Gly	Arg	Val	Val	Ala	Gly	Val	Ala	Ser	Gly	Leu	Ala	Lys	His					
	55					60					65									
ctt	aat	gtg	tcg	gtg	ttt	tgg	gtt	cgt	gcg	ctg	ctg	att	ttt	gcg	gcg	355				
Leu	Asn	Val	Ser	Val	Phe	Trp	Val	Arg	Ala	Leu	Leu	Ile	Phe	Ala	Ala					
70					75					80					85					
ttg	ctg	agc	ggt	gcg	ggt	ctt	ttt	gcg	tat	gcc	ttg	att	tgg	att	ttt	403				
Leu	Leu	Ser	Gly	Ala	Gly	Leu	Phe	Ala	Tyr	Ala	Leu	Ile	Trp	Ile	Phe					
				90				95						100						
acg	cgc	att	gag	aaa	aag	ggg	agt	ggg	gag	gcg	tcg	aca	agc	aag	cgc	451				
Thr	Arg	Ile	Glu	Lys	Lys	Gly	Ser	Gly	Glu	Ala	Ser	Thr	Ser	Lys	Arg					
			105					110					115							
tgg	gtg	tcg	tgg	tgc	ctg	gtg	ctg	ctc	gct	atc	ggt	ggt	gct	gcg	gcg	499				
Trp	Val	Ser	Trp	Cys	Leu	Val	Leu	Leu	Ala	Ile	Gly	Gly	Ala	Ala	Ala					
	120						125					130								
tcg	gtg	atg	ctg	agc	acc	ggc	ttc	gcg	gtg	ggc	acg	ttg	gtg	ccc	atc	547				
Ser	Val	Met	Leu	Ser	Thr	Gly	Phe	Ala	Val	Gly	Thr	Leu	Val	Pro	Ile					
	135					140					145									
ggc	gtg	gtc	ggt	gtg	ggc	ctg	ttg	atg	gtg	tgg	ctg	gcg	tat	gac	cgc	595				
Gly	Val	Val	Gly	Val	Gly	Leu	Leu	Met	Val	Trp	Leu	Ala	Tyr	Asp	Arg					
150					155					160					165					
ggg	gtg	gaa	tcc	ggc	ccg	aat	ctg	ctg	att	att	gcc	acc	ggc	ggt	gtg	643				
Gly	Val	Glu	Ser	Gly	Pro	Asn	Leu	Leu	Ile	Ile	Ala	Thr	Gly	Gly	Val					
				170					175					180						
ttg	atg	ctg	gtg	gcg	atc	gtg	ctg	atc	gtg	atg	aat	tgg	aac	acc	cag	691				
Leu	Met	Leu	Val	Ala	Ile	Val	Leu	Ile	Val	Met	Asn	Trp	Asn	Thr	Gln					
			185					190					195							
gac	ggc	ttc	gtc	atg	gcg	ctg	gtg	gcc	gtg	gtg	ctc	acg	ctg	gtg	ggt	739				
Asp	Gly	Phe	Val	Met	Ala	Leu	Val	Ala	Val	Val	Leu	Thr	Leu	Val	Gly					
		200					205					210								
gtg	gct	gcg	ctg	ggc	gtt	ccg	ctg	tgg	gtg	cgg	atg	tgg	gat	cag	ctg	787				
Val	Ala	Ala	Leu	Gly	Val	Pro	Leu	Trp	Val	Arg	Met	Trp	Asp	Gln	Leu					
	215					220					225									
ggc	gag	gag	cgc	gcg	gaa	aaa	gcc	gca	gct	gct	gag	cgc	gca	gat	att	835				
Gly	Glu	Glu	Arg	Ala	Glu	Lys	Ala	Ala	Ala	Ala	Glu	Arg	Ala	Asp	Ile					
230					235					240					245					
gct	tcc	cgc	ctg	cat	gat	tcg	gta	ctg	cag	acc	ttg	gcg	ctg	att	caa	883				
Ala	Ser	Arg	Leu	His	Asp	Ser	Val	Leu	Gln	Thr	Leu	Ala	Leu	Ile	Gln					
				250					255					260						
aag	cgt	gcc	gac	gac	ccc	gcc	gaa	gtc	gcc	cgc	ctg	gcc	cgc	ggg	cag	931				
Lys	Arg	Ala	Asp	Asp	Pro	Ala	Glu	Val	Ala	Arg	Leu	Ala	Arg	Gly	Gln					
			265					270						275						

gaa cgc gag ctg cgt caa tgg ctg ttt gat tcc caa gat aaa aca cct 979
 Glu Arg Glu Leu Arg Gln Trp Leu Phe Asp Ser Gln Asp Lys Thr Pro
 280 285 290

caa aca acc ggc act gtc ttt act gcg ttg gag cgc gcc tgc ggt gaa 1027
 Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu Arg Ala Cys Gly Glu
 295 300 305

gtc gag gat att tac gct ctg cgt atc gtg cct gtg acc gtg gga acc 1075
 Val Glu Asp Ile Tyr Ala Leu Arg Ile Val Pro Val Thr Val Gly Thr
 310 315 320 325

gat gaa gcg ctg act gag aaa acg cag gca gcg gtg atg gca gtc cgc 1123
 Asp Glu Ala Leu Thr Glu Lys Thr Gln Ala Val Met Ala Val Arg
 330 335 340

gaa gca ctc gtg aac gtg gcc aag cat gcc ggc gtg gaa acc gcc gat 1171
 Glu Ala Leu Val Asn Val Ala Lys His Ala Gly Val Glu Thr Ala Asp
 345 350 355

gtg tac gcc gaa att atg ctc ggc gaa ctg aac att ttc gtc cgc gac 1219
 Val Tyr Ala Glu Ile Met Leu Gly Glu Leu Asn Ile Phe Val Arg Asp
 360 365 370

cgc ggt gca gga ttc gac ccc gac aac atc ccc gac ggg cac cac ggg 1267
 Arg Gly Ala Gly Phe Asp Pro Asp Asn Ile Pro Asp Gly His His Gly
 375 380 385

ctc gcc gaa tcc gtc caa ggc cgc gtc gaa cga gcc ggc gga aaa gta 1315
 Leu Ala Glu Ser Val Gln Gly Arg Val Glu Arg Ala Gly Gly Lys Val
 390 395 400 405

cgc atc aaa tct gaa atc ggc gaa ggc acc gaa gtg gca atc acc atg 1363
 Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu Val Ala Ile Thr Met
 410 415 420

gat gtg tagttggtcg tacgcgcgtg tct 1392
 Asp Val

<210> 304

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Gly Glu Ser Pro Glu Lys Val Ala Phe Arg Val Phe Pro Asp Gly
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Leu Val Ser Gln Gly His Asp Met Ile Glu Asp Met Ser Asn Thr Pro
20 25 30

Ala Pro Tyr Thr Pro Gln Pro Ala Gly Gln Ala Val Pro Leu Tyr Pro
35 40 45

Thr Phe Thr Arg Ser Arg Asp Gly Arg Val Val Ala Gly Val Ala Ser
50 55 60

Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu

65					70					75					80
Leu	Ile	Phe	Ala	Ala	Leu	Leu	Ser	Gly	Ala	Gly	Leu	Phe	Ala	Tyr	Ala
				85					90					95	
Leu	Ile	Trp	Ile	Phe	Thr	Arg	Ile	Glu	Lys	Lys	Gly	Ser	Gly	Glu	Ala
			100					105					110		
Ser	Thr	Ser	Lys	Arg	Trp	Val	Ser	Trp	Cys	Leu	Val	Leu	Leu	Ala	Ile
		115					120					125			
Gly	Gly	Ala	Ala	Ala	Ser	Val	Met	Leu	Ser	Thr	Gly	Phe	Ala	Val	Gly
	130					135					140				
Thr	Leu	Val	Pro	Ile	Gly	Val	Val	Gly	Val	Gly	Leu	Leu	Met	Val	Trp
145					150					155					160
Leu	Ala	Tyr	Asp	Arg	Gly	Val	Glu	Ser	Gly	Pro	Asn	Leu	Leu	Ile	Ile
				165					170					175	
Ala	Thr	Gly	Gly	Val	Leu	Met	Leu	Val	Ala	Ile	Val	Leu	Ile	Val	Met
			180					185					190		
Asn	Trp	Asn	Thr	Gln	Asp	Gly	Phe	Val	Met	Ala	Leu	Val	Ala	Val	Val
		195					200					205			
Leu	Thr	Leu	Val	Gly	Val	Ala	Ala	Leu	Gly	Val	Pro	Leu	Trp	Val	Arg
	210					215					220				
Met	Trp	Asp	Gln	Leu	Gly	Glu	Glu	Arg	Ala	Glu	Lys	Ala	Ala	Ala	Ala
225					230					235					240
Glu	Arg	Ala	Asp	Ile	Ala	Ser	Arg	Leu	His	Asp	Ser	Val	Leu	Gln	Thr
				245					250					255	
Leu	Ala	Leu	Ile	Gln	Lys	Arg	Ala	Asp	Asp	Pro	Ala	Glu	Val	Ala	Arg
			260					265					270		
Leu	Ala	Arg	Gly	Gln	Glu	Arg	Glu	Leu	Arg	Gln	Trp	Leu	Phe	Asp	Ser
		275					280					285			
Gln	Asp	Lys	Thr	Pro	Gln	Thr	Thr	Gly	Thr	Val	Phe	Thr	Ala	Leu	Glu
	290					295					300				
Arg	Ala	Cys	Gly	Glu	Val	Glu	Asp	Ile	Tyr	Ala	Leu	Arg	Ile	Val	Pro
305					310					315					320
Val	Thr	Val	Gly	Thr	Asp	Glu	Ala	Leu	Thr	Glu	Lys	Thr	Gln	Ala	Ala
				325					330					335	
Val	Met	Ala	Val	Arg	Glu	Ala	Leu	Val	Asn	Val	Ala	Lys	His	Ala	Gly
			340					345					350		
Val	Glu	Thr	Ala	Asp	Val	Tyr	Ala	Glu	Ile	Met	Leu	Gly	Glu	Leu	Asn
		355					360					365			
Ile	Phe	Val	Arg	Asp	Arg	Gly	Ala	Gly	Phe	Asp	Pro	Asp	Asn	Ile	Pro
	370					375					380				
Asp	Gly	His	His	Gly	Leu	Ala	Glu	Ser	Val	Gln	Gly	Arg	Val	Glu	Arg
385					390					395					400

Ala Gly Gly Lys Val Arg Ile Lys Ser Glu Ile Gly Glu Gly Thr Glu
 405 410 415

Val Ala Ile Thr Met Asp Val
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<210> 305

<211> 813

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(790)

<223> RXS00471

<400> 305

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ggtcgtacgc gcgtgtcttc ggggctgtaa cctgaaaggc atg gtt gat gtg ttt 115
 Met Val Asp Val Phe
 1 5

ttg gtc gat gac cac tcc gtg ttt cgc tcc ggc gtc aaa gca gaa cta 163
 Leu Val Asp Asp His Ser Val Phe Arg Ser Gly Val Lys Ala Glu Leu
 10 15 20

ggc aac gcc gtc aca gta gtc ggc gaa gca ggg acg gtg gcc gac gcc 211
 Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly Thr Val Ala Asp Ala
 25 30 35

gta gcc ggc atc aag gca agc aaa cca gag gta gtg ctt ctc gac gtc 259
 Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val Val Leu Leu Asp Val
 40 45 50

cac atg ccc gac ggc ggc ggc ctc gca gtg ctc cag cag atc aac gac 307
 His Met Pro Asp Gly Gly Gly Leu Ala Val Leu Gln Gln Ile Asn Asp
 55 60 65

tcc gat gtg gac acc att ttc ttg gca ctc agt gtc tct gat gct gcg 355
 Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser Val Ser Asp Ala Ala
 70 75 80 85

gaa gat gtc atc gcc atc atc cgt ggc ggt gcc agg gga tac gtg acc 403
 Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala Arg Gly Tyr Val Thr
 90 95 100

aaa tca atc tcc ggt gaa gaa ctc atc gaa gcc atc aac cgc gtg aaa 451
 Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala Ile Asn Arg Val Lys
 105 110 115

tcc ggc gac gca ttc ttc tca cca cgc ctg gca ggc ttt gtc ctc gac 499
 Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala Gly Phe Val Leu Asp
 120 125 130

gcc ttc gcc gcc ccc gat tcc gca gct ggc gca ggc att gtc gac gca 547
 Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala Gly Ile Val Asp Ala
 135 140 145

ccc gaa aaa gac gcc gcc gta gaa tcc gga aaa atc ctc gac gac cca 595
 Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys Ile Leu Asp Asp Pro
 150 155 160 165

gtt gtc gac gcc ctc acc cgc cgc gaa ctc gaa gtc ctc cgc cta cta 643
 Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu Val Leu Arg Leu Leu
 170 175 180

gcc cgc ggc tac acc tac aaa gaa atc ggc aaa gaa ctg ttc att tcc 691
 Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys Glu Leu Phe Ile Ser
 185 190 195

gtc aaa acc gtg gaa acc cac gcc tca aac att ctg cgg aaa acc caa 739
 Val Lys Thr Val Glu Thr His Ala Ser Asn Ile Leu Arg Lys Thr Gln
 200 205 210

caa tcc aac cgc cac gcg ttg acc cgg tgg gct cac tcg agg gat ctt 787
 Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala His Ser Arg Asp Leu
 215 220 225

gac taatggcggc taaaaagagt ggc 813
 Asp
 230

<210> 306

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Met Val Asp Val Phe Leu Val Asp Asp His Ser Val Phe Arg Ser Gly
 1 5 10 15

Val Lys Ala Glu Leu Gly Asn Ala Val Thr Val Val Gly Glu Ala Gly
 20 25 30

Thr Val Ala Asp Ala Val Ala Gly Ile Lys Ala Ser Lys Pro Glu Val
 35 40 45

Val Leu Leu Asp Val His Met Pro Asp Gly Gly Gly Leu Ala Val Leu
 50 55 60

Gln Gln Ile Asn Asp Ser Asp Val Asp Thr Ile Phe Leu Ala Leu Ser
 65 70 75 80

Val Ser Asp Ala Ala Glu Asp Val Ile Ala Ile Ile Arg Gly Gly Ala
 85 90 95

Arg Gly Tyr Val Thr Lys Ser Ile Ser Gly Glu Glu Leu Ile Glu Ala
 100 105 110

Ile Asn Arg Val Lys Ser Gly Asp Ala Phe Phe Ser Pro Arg Leu Ala
 115 120 125

Gly Phe Val Leu Asp Ala Phe Ala Ala Pro Asp Ser Ala Ala Gly Ala
 130 135 140

Gly Ile Val Asp Ala Pro Glu Lys Asp Ala Ala Val Glu Ser Gly Lys
 145 150 155 160

Ile Leu Asp Asp Pro Val Val Asp Ala Leu Thr Arg Arg Glu Leu Glu
 165 170 175

Val Leu Arg Leu Leu Ala Arg Gly Tyr Thr Tyr Lys Glu Ile Gly Lys
 180 185 190

Glu Leu Phe Ile Ser Val Lys Thr Val Glu Thr His Ala Ser Asn Ile
 195 200 205

Leu Arg Lys Thr Gln Gln Ser Asn Arg His Ala Leu Thr Arg Trp Ala
 210 215 220

His Ser Arg Asp Leu Asp
 225 230

<210> 307
 <211> 708
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(685)
 <223> RXS00481

<400> 307
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aaataaaactt tatctgactt tgtagaaaaa ggtgattact atg ctg aat atg cag 115
 Met Leu Asn Met Gln
 1 5

gaa cca gat aaa atc cat ccg gca gaa cct aca ctt cgt aat att tat 163
 Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr Leu Arg Asn Ile Tyr
 10 15 20

gac gtt aaa act agt gat ccc aaa agt gaa tta gtt gat cgt tct ggc 211
 Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu Val Asp Arg Ser Gly
 25 30 35

atg tcg gaa gaa gac att gcg caa att ggg cgg cta atg aaa tcg ttg 259
 Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg Leu Met Lys Ser Leu
 40 45 50

gcc agt ctt cgc gat gtg gaa cgt agt att ggt gaa gcc tcg gca cgt 307
 Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly Glu Ala Ser Ala Arg
 55 60 65

tat atg gag cta agt gcc cct gat atg cga gct ttg cac tat ttg att 355
 Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala Leu His Tyr Leu Ile
 70 75 80 85

gtg gcg ggc aat gcg ggc gaa gtg gtg act cca gga atg ctt gga gct 403
 Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro Gly Met Leu Gly Ala
 90 95 100

cac ctt aag ctt tcc ccg gca tct gta aca aag acg ctt aat agg cta 451
 His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys Thr Leu Asn Arg Leu
 105 110 115

gaa aaa ggt ggg cat att gtt cgt aat gtg cac ccc gtc gac cgc agg 499
 Glu Lys Gly Gly His Ile Val Arg Asn Val His Pro Val Asp Arg Arg
 120 125 130

gct ttc gcc ctc atg gtc act gat gcc act cgt gga gag gcg atg cgg 547
 Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg Gly Glu Ala Met Arg
 135 140 145

acg ctt ggt aag cat cag gcg cgt cgt ttt gat gct gct aaa cga tta 595
 Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp Ala Ala Lys Arg Leu
 150 155 160 165

act cca caa gag cgt gaa gtg gtt atc cga ttc ctt cag gat atg gca 643
 Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe Leu Gln Asp Met Ala
 170 175 180

cag gag tta tcc ctt aat aat gca cca tgg ctc aac acg gag 685
 Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu Asn Thr Glu
 185 190 195

tagatgacca tctacgttaa tta 708

<210> 308
 <211> 195
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 308
 Met Leu Asn Met Gln Glu Pro Asp Lys Ile His Pro Ala Glu Pro Thr
 1 5 10 15

Leu Arg Asn Ile Tyr Asp Val Lys Thr Ser Asp Pro Lys Ser Glu Leu
 20 25 30

Val Asp Arg Ser Gly Met Ser Glu Glu Asp Ile Ala Gln Ile Gly Arg
 35 40 45

Leu Met Lys Ser Leu Ala Ser Leu Arg Asp Val Glu Arg Ser Ile Gly
 50 55 60

Glu Ala Ser Ala Arg Tyr Met Glu Leu Ser Ala Pro Asp Met Arg Ala
 65 70 75 80

Leu His Tyr Leu Ile Val Ala Gly Asn Ala Gly Glu Val Val Thr Pro
 85 90 95

Gly Met Leu Gly Ala His Leu Lys Leu Ser Pro Ala Ser Val Thr Lys
 100 105 110

Thr Leu Asn Arg Leu Glu Lys Gly Gly His Ile Val Arg Asn Val His
 115 120 125

Pro Val Asp Arg Arg Ala Phe Ala Leu Met Val Thr Asp Ala Thr Arg
 130 135 140

Gly Glu Ala Met Arg Thr Leu Gly Lys His Gln Ala Arg Arg Phe Asp
 145 150 155 160

Ala Ala Lys Arg Leu Thr Pro Gln Glu Arg Glu Val Val Ile Arg Phe
 165 170 175

Leu Gln Asp Met Ala Gln Glu Leu Ser Leu Asn Asn Ala Pro Trp Leu
 180 185 190

Asn Thr Glu
 195

<210> 309

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXS00649

<400> 309

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cattttgtgc aagatgcaat agctggcaaa ctggagagcc atg agc acc gac ccc 115
 Met Ser Thr Asp Pro
 1 5

atc gcg gcc ttg gaa tac gaa tcc acc atc ttc gcc cgt cac cgg aat 163
 Ile Ala Ala Leu Glu Tyr Glu Ser Thr Ile Phe Ala Arg His Arg Asn
 10 15 20

caa tac acc ggc caa gca ggt acg aat gct ggc gtc ctc gat tcc agc 211
 Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly Val Leu Asp Ser Ser
 25 30 35

ggc tac aac cta ctc acg ctg ctc cag tta cgt ggc ccc tcc acc atc 259
 Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg Gly Pro Ser Thr Ile
 40 45 50

ggc gaa ctc agc gcc atc acc ggc cta gac gca tct acc ctt aac cgt 307
 Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala Ser Thr Leu Asn Arg
 55 60 65

cag aca aaa gcc cta cta acc aaa gga ttt gtc gaa cgc atc cca gat 355
 Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val Glu Arg Ile Pro Asp
 70 75 80 85

ccc gac ggt gga atc gct cgg aaa ttc cac ccc acc gac ctc ggc aat 403
 Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro Thr Asp Leu Gly Asn
 90 95 100

gaa ctg ctc aac gag gaa cgc aca tcc agc caa gaa aaa tat gcc gag 451
 Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln Glu Lys Tyr Ala Glu
 105 110 115

tta ctt tca gac tgg ccc gaa gag gat cta cgc acc ttc gtc aaa ctt 499
 Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg Thr Phe Val Lys Leu
 120 125 130

ctt gaa aaa cta aat aaa gcc gtg gag aca cgc gtc gga aag cat tgg 547
 Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg Val Gly Lys His Trp
 135 140 145

cgc cgc ccc tgactcagcc caagccagag ccc
 Pro Arg Pro
 150

579

<210> 310
 <211> 152
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 310
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 Ala Arg His Arg Asn Gln Tyr Thr Gly Gln Ala Gly Thr Asn Ala Gly
 20 25 30
 Val Leu Asp Ser Ser Gly Tyr Asn Leu Leu Thr Leu Leu Gln Leu Arg
 35 40 45
 Gly Pro Ser Thr Ile Gly Glu Leu Ser Ala Ile Thr Gly Leu Asp Ala
 50 55 60
 Ser Thr Leu Asn Arg Gln Thr Lys Ala Leu Leu Thr Lys Gly Phe Val
 65 70 75 80
 Glu Arg Ile Pro Asp Pro Asp Gly Gly Ile Ala Arg Lys Phe His Pro
 85 90 95
 Thr Asp Leu Gly Asn Glu Leu Leu Asn Glu Glu Arg Thr Ser Ser Gln
 100 105 110
 Glu Lys Tyr Ala Glu Leu Leu Ser Asp Trp Pro Glu Glu Asp Leu Arg
 115 120 125
 Thr Phe Val Lys Leu Leu Glu Lys Leu Asn Lys Ala Val Glu Thr Arg
 130 135 140
 Val Gly Lys His Trp Pro Arg Pro
 145 150

<210> 311
 <211> 759
 <212> DNA
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<220>
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 <222> (101)..(736)
 <223> RXS00650

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 Met Ile Arg Val Leu
 1 5
 ctt gct gat gac cac gaa atc gtg agg ctc gga ctc cga gct gtg ctg 163
 Leu Ala Asp Asp His Glu Ile Val Arg Leu Gly Leu Arg Ala Val Leu

10										15					20					
gaa agc gcc gag gac att gaa gtg gtg ggc gaa gtc tcc acc gcc gaa	211																			
Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu Val Ser Thr Ala Glu																				
25 30 35																				
ggt gcg gtg cag gca gcc caa gaa ggc gga atc gac gtc atc ttg atg	259																			
Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile Asp Val Ile Leu Met																				
40 45 50																				
gac ctc cga ttc ggc ccc ggc gtc caa gga acc cag gtt tcc aca ggc	307																			
Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr Gln Val Ser Thr Gly																				
55 60 65																				
gca gac gcc acc gca gcc atc aag cga aac atc gat aac ccg cca aaa	355																			
Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile Asp Asn Pro Pro Lys																				
70 75 80 85																				
gtc ctg gtc gtg acc aac tac gac acc gac aca gac atc ctc ggc gca	403																			
Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr Asp Ile Leu Gly Ala																				
90 95 100																				
atc gaa gcc ggc gca ctg ggc tac ctg ctc aaa gac gcc cca ccg agc	451																			
Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys Asp Ala Pro Pro Ser																				
105 110 115																				
gaa ctc ctg gca gca gta cga tcc gca gca gaa ggt gac tcc aca ctg	499																			
Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu Gly Asp Ser Thr Leu																				
120 125 130																				
tca ccc atg gtt gcg aac cgc ctg atg act cgc gtg cgc acc ccc aaa	547																			
Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg Val Arg Thr Pro Lys																				
135 140 145																				
acc tca ctc acc cca cgt gaa ctg gaa gtt ctc aag ctg gtt gcc ggt	595																			
Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu Lys Leu Val Ala Gly																				
150 155 160 165																				
gga tcc tcc aac cgc gac att ggc cgt atc ctc ttc ctc tca gaa gcc	643																			
Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu Phe Leu Ser Glu Ala																				
170 175 180																				
acg gtg aaa tcc cac ctc gtg cac atc tac gac aag ctc ggc gtg cgg	691																			
Thr Val Lys Ser His Leu Val His Ile Tyr Asp Lys Leu Gly Val Arg																				
185 190 195																				
tca cgt acc tcc gct gtc gca gcc gca cgt gag cag ggg ctg ctg	736																			
Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu Gln Gly Leu Leu																				
200 205 210																				
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<210> 312

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

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Leu Arg Ala Val Leu Glu Ser Ala Glu Asp Ile Glu Val Val Gly Glu
 20 25 30
 Val Ser Thr Ala Glu Gly Ala Val Gln Ala Ala Gln Glu Gly Gly Ile
 35 40 45
 Asp Val Ile Leu Met Asp Leu Arg Phe Gly Pro Gly Val Gln Gly Thr
 50 55 60
 Gln Val Ser Thr Gly Ala Asp Ala Thr Ala Ala Ile Lys Arg Asn Ile
 65 70 75 80
 Asp Asn Pro Pro Lys Val Leu Val Val Thr Asn Tyr Asp Thr Asp Thr
 85 90 95
 Asp Ile Leu Gly Ala Ile Glu Ala Gly Ala Leu Gly Tyr Leu Leu Lys
 100 105 110
 Asp Ala Pro Pro Ser Glu Leu Leu Ala Ala Val Arg Ser Ala Ala Glu
 115 120 125
 Gly Asp Ser Thr Leu Ser Pro Met Val Ala Asn Arg Leu Met Thr Arg
 130 135 140
 Val Arg Thr Pro Lys Thr Ser Leu Thr Pro Arg Glu Leu Glu Val Leu
 145 150 155 160
 Lys Leu Val Ala Gly Gly Ser Ser Asn Arg Asp Ile Gly Arg Ile Leu
 165 170 175
 Phe Leu Ser Glu Ala Thr Val Lys Ser His Leu Val His Ile Tyr Asp
 180 185 190
 Lys Leu Gly Val Arg Ser Arg Thr Ser Ala Val Ala Ala Ala Arg Glu
 195 200 205
 Gln Gly Leu Leu
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<210> 313
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1003)
 <223> RXS00657

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 Met Ser Thr Glu Asp
 1 5
 att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt 163
 Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
 10 15 20

cg	g	t	g	g	c	t	a	a	a	c	c	a	c	t	c	g	t	t	g	211
Arg	Trp	Ala	Ala	Asn	Thr	Ala	Asn	Lys	Arg	Gly	Ile	Pro	Leu	Arg	Leu					
		25						30					35							
g	c	t	t	a	c	c	a	t	t	c	t	a	c	g	a	g	a	t	g	259
Ala	Ser	Ser	Tyr	Thr	Met	Pro	Gln	Phe	Leu	Tyr	Ala	Glu	Gly	Met	Val					
		40					45					50								
c	c	a	a	g	a	t	t	c	a	t	c	c	a	g	a	a	a	a	g	307
Pro	Pro	Gln	Glu	Leu	Phe	Asp	Asp	Leu	Gln	Ala	Glu	Ala	Leu	Glu	Lys					
		55				60					65									
a	a	c	a	a	g	c	c	a	t	c	a	t	c	a	a	a	a	a	g	355
Ile	Asn	Glu	Ala	Arg	Asp	Ile	Ala	His	Glu	Val	Ala	Pro	Glu	Ile	Lys					
70					75				80						85					
a	t	c	c	a	c	a	t	c	g	a	a	g	a	c	a	a	a	a	g	403
Ile	Gly	His	Thr	Ile	Ala	Glu	Gly	Ser	Pro	Ile	Asp	Met	Leu	Leu	Glu					
			90						95				100							
a	t	c	c	a	a	g	a	c	a	t	c	c	a	a	a	a	a	a	g	451
Met	Ser	Pro	Asp	Ala	Thr	Met	Ile	Val	Met	Gly	Ser	Arg	Gly	Leu	Gly					
			105					110					115							
g	a	a	c	a	a	g	a	t	c	c	a	a	a	a	a	a	a	a	g	499
Gly	Leu	Ser	Gly	Met	Val	Met	Gly	Ser	Val	Ser	Gly	Ala	Val	Val	Ser					
		120					125					130								
c	a	c	a	a	a	g	a	t	c	c	a	a	a	a	a	a	a	a	g	547
His	Ala	Lys	Cys	Pro	Val	Val	Val	Val	Arg	Glu	Asp	Ser	Ala	Val	Asn					
		135				140					145									
g	a	a	a	a	a	g	a	t	c	c	a	a	a	a	a	a	a	a	g	595
Glu	Asp	Ser	Lys	Tyr	Gly	Pro	Val	Val	Val	Gly	Val	Asp	Gly	Ser	Glu					
150					155					160					165					
g	t	c	c	a	a	g	a	t	c	c	a	a	a	a	a	a	a	a	g	643
Val	Ser	Gln	Gln	Ala	Thr	Glu	Tyr	Ala	Phe	Ala	Glu	Ala	Glu	Ala	Arg					
				170					175					180						
g	g	c	a	a	c	t	c	a	a	c	t	c	a	a	a	a	a	a	g	691
Gly	Ala	Glu	Leu	Val	Ala	Val	His	Thr	Trp	Met	Asp	Met	Gln	Val	Gln					
			185					190					195							
g	c	a	c	t	c	a	a	c	a	c	a	c	a	a	a	a	a	a	g	739
Ala	Ser	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Gln	Gln	Gln	Trp	Asp	Glu	Val					
		200				205						210								
g	a	a	c	a	a	g	a	c	a	c	c	c	a	c	a	a	a	a	g	787
Glu	Arg	Gln	Gln	Thr	Asp	Met	Leu	Ile	Glu	Arg	Leu	Ala	Pro	Leu	Val					
	215				220						225									
g	a	a	a	a	a	g	a	a	a	a	a	a	a	a	a	a	a	a	g	835
Glu	Lys	Tyr	Pro	Ser	Val	Thr	Val	Lys	Lys	Ile	Ile	Thr	Arg	Asp	Arg					
230					235				240						245					
c	c	a	a	a	a	g	a	a	a	a	a	a	a	a	a	a	a	a	g	883
Pro	Val	Arg	Ala	Leu	Ala	Glu	Ala	Ser	Glu	Asn	Ala	Gln	Leu	Leu	Val					
				250					255					260						

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
 Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
 265 270 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
 Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
 280 285 290

cgc cca cct gag aag att aag aag tagttttcttt taagtttcga tgc 1026
 Arg Pro Pro Glu Lys Ile Lys Lys
 295 300

<210> 314

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

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Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
 20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
 35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
 50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
 85 90 95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
 165 170 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
 180 185 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
 195 200 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
 245 250 255
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270
 Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285
 Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

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 <222> (101)..(1729)
 <223> RXS00719

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 tcattccacct agtgggaagcc tccgctgaaa ggagcaacca gtg act gat aaa cac 115
 Val Thr Asp Lys His
 1 5
 acc atg cct ggt gaa gag gac gac acc gta ttc gtc tac cac acc cac 163
 Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe Val Tyr His Thr His
 10 15 20
 aaa ggc gaa atg gac gtc gaa ggt gcg ttt gct gac gaa gaa gaa cta 211
 Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala Asp Glu Glu Glu Leu
 25 30 35
 gca cca cac ggc ggt tgg gct tcc gca gat ttc gac cca gca gaa ttc 259
 Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe Asp Pro Ala Glu Phe
 40 45 50
 ggc tac gaa gac tct gac gat gac ttc gat gca gag gac ttt gac gaa 307
 Gly Tyr Glu Asp Ser Asp Asp Phe Asp Ala Glu Asp Phe Asp Glu
 55 60 65
 aca gag ttc tcc aac cct gat ttc ggc gaa gac tac tct gat gaa gac 355
 Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp Tyr Ser Asp Glu Asp
 70 75 80 85
 tgg gaa gaa atc gag acc gca ttc gga ttc gac cca agc cac ctt gaa 403
 Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp Pro Ser His Leu Glu
 90 95 100
 gaa gct ctc tgc acg gtc gct atc gtc gga cgc cca aat gtt ggt aaa 451
 Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg Pro Asn Val Gly Lys
 105 110 115

tca acc ttg gtg aac cgc ttt att gga cgt cga gaa gca gtc gtg gaa	499
Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu	
120 125 130	
gat ttc ccc ggc gta acc cgt gac cgc atc tcc tac atc tct gac tgg	547
Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp	
135 140 145	
ggg gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac	595
Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn	
150 155 160 165	
gtc aag ggc atc cac gca tcg atc gca cag caa gca gaa gtt gct atg	643
Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln Ala Glu Val Ala Met	
170 175 180	
agc act gcc gat gtc atc gta ttc gtc gtg gac acc aag gtg ggc atc	691
Ser Thr Ala Asp Val Ile Val Phe Val Val Asp Thr Lys Val Gly Ile	
185 190 195	
acc gaa act gac tca gtg atg gca gca aaa ctg ttg cgc tcg gaa gtg	739
Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu Leu Arg Ser Glu Val	
200 205 210	
cca gtg atc ttg gtt gcg aac aaa ttc gac tcc gac agc cag tgg gct	787
Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser Asp Ser Gln Trp Ala	
215 220 225	
gac atg gct gag ttc tac agc ctc ggc ctt ggc gat cca tac cca gtt	835
Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly Asp Pro Tyr Pro Val	
230 235 240 245	
tca gcc cag cat gga cgt ggt ggc gct gac gtt ttg gac aaa gtc ctt	883
Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val Leu Asp Lys Val Leu	
250 255 260	
gaa ctc ttc cca gaa gag cct cgc tcc aag tcc atc gtg gaa ggc cct	931
Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser Ile Val Glu Gly Pro	
265 270 275	
cgt cgt gtc gcc ctt gtg ggt aag cca aac gtg ggt aag tct tca ctg	979
Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val Gly Lys Ser Ser Leu	
280 285 290	
ctc aac aag ttt gct ggc gag acc cgc tct gtc gtg gac aat gtt gca	1027
Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val Val Asp Asn Val Ala	
295 300 305	
gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa	1075
Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys	
310 315 320 325	
ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act	1123
Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr	
330 335 340	
gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc	1171
Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile	
345 350 355	
gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc	1219

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Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile
    360                      365                      370

acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag 1267
Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys
    375                      380                      385

gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc 1315
Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg
    390                      395                      400                      405

cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct 1363
Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro
    410                      415                      420

tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag 1411
Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln
    425                      430                      435

cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt 1459
Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg
    440                      445                      450

atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg 1507
Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala
    455                      460                      465

aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc 1555
Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala
    470                      475                      480                      485

acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc 1603
Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly
    490                      495                      500

ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa 1651
Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
    505                      510                      515

cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc 1699
Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
    520                      525                      530

gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttcctaa aag 1752
Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
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<210> 316

<211> 543

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
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Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
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Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe

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35					40					45					
Asp	Pro	Ala	Glu	Phe	Gly	Tyr	Glu	Asp	Ser	Asp	Asp	Asp	Phe	Asp	Ala
50						55					60				
Glu	Asp	Phe	Asp	Glu	Thr	Glu	Phe	Ser	Asn	Pro	Asp	Phe	Gly	Glu	Asp
65					70					75					80
Tyr	Ser	Asp	Glu	Asp	Trp	Glu	Glu	Ile	Glu	Thr	Ala	Phe	Gly	Phe	Asp
				85					90					95	
Pro	Ser	His	Leu	Glu	Glu	Ala	Leu	Cys	Thr	Val	Ala	Ile	Val	Gly	Arg
			100					105					110		
Pro	Asn	Val	Gly	Lys	Ser	Thr	Leu	Val	Asn	Arg	Phe	Ile	Gly	Arg	Arg
			115				120						125		
Glu	Ala	Val	Val	Glu	Asp	Phe	Pro	Gly	Val	Thr	Arg	Asp	Arg	Ile	Ser
			130				135					140			
Tyr	Ile	Ser	Asp	Trp	Gly	Gly	His	Arg	Phe	Trp	Val	Gln	Asp	Thr	Gly
145					150					155					160
Gly	Trp	Asp	Pro	Asn	Val	Lys	Gly	Ile	His	Ala	Ser	Ile	Ala	Gln	Gln
				165					170					175	
Ala	Glu	Val	Ala	Met	Ser	Thr	Ala	Asp	Val	Ile	Val	Phe	Val	Val	Asp
			180					185					190		
Thr	Lys	Val	Gly	Ile	Thr	Glu	Thr	Asp	Ser	Val	Met	Ala	Ala	Lys	Leu
		195					200					205			
Leu	Arg	Ser	Glu	Val	Pro	Val	Ile	Leu	Val	Ala	Asn	Lys	Phe	Asp	Ser
	210					215					220				
Asp	Ser	Gln	Trp	Ala	Asp	Met	Ala	Glu	Phe	Tyr	Ser	Leu	Gly	Leu	Gly
225					230					235					240
Asp	Pro	Tyr	Pro	Val	Ser	Ala	Gln	His	Gly	Arg	Gly	Gly	Ala	Asp	Val
				245					250					255	
Leu	Asp	Lys	Val	Leu	Glu	Leu	Phe	Pro	Glu	Glu	Pro	Arg	Ser	Lys	Ser
			260					265					270		
Ile	Val	Glu	Gly	Pro	Arg	Arg	Val	Ala	Leu	Val	Gly	Lys	Pro	Asn	Val
		275					280					285			
Gly	Lys	Ser	Ser	Leu	Leu	Asn	Lys	Phe	Ala	Gly	Glu	Thr	Arg	Ser	Val
	290					295					300				
Val	Asp	Asn	Val	Ala	Gly	Thr	Thr	Val	Asp	Pro	Val	Asp	Ser	Leu	Ile
305					310					315					320
Gln	Leu	Asp	Gln	Lys	Leu	Trp	Lys	Phe	Val	Asp	Thr	Ala	Gly	Leu	Arg
				325					330					335	
Lys	Lys	Val	Lys	Thr	Ala	Ser	Gly	His	Glu	Tyr	Tyr	Ala	Ser	Leu	Arg
			340					345					350		
Thr	His	Gly	Ala	Ile	Asp	Ala	Ala	Glu	Leu	Cys	Val	Leu	Leu	Ile	Asp
		355					360					365			

Ser Ser Glu Pro Ile Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile
 370 375 380
 Thr Asp Ala Gly Lys Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu
 385 390 395 400
 Met Asp Glu Asp Arg Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln
 405 410 415
 Leu Ala His Val Pro Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr
 420 425 430
 Gly Arg Ala Leu Gln Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp
 435 440 445
 Asn Trp Asp Arg Arg Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg
 450 455 460
 Glu Ala Ile Ala Ala Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro
 465 470 475 480
 Arg Val Leu Phe Ala Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val
 485 490 495
 Leu Phe Thr Thr Gly Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu
 500 505 510
 Arg Lys Phe Arg Glu Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile
 515 520 525
 Ala Val Arg Val Arg Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
 530 535 540

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<211> 386

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(363)

<223> RXS00738

<400> 317

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Cys	Gln	Glu	Glu	Thr	Asp	Gly	Phe	Phe	Asp	Phe	Gly	Arg	Asp	Met	Arg	
1				5					10					15		
ccc	ggt	gag	cgc	cgg	tcg	tat	ggc	act	ttg	ctt	aac	gac	gcc	acg	acg	96
Pro	Gly	Glu	Arg	Arg	Ser	Tyr	Gly	Thr	Leu	Leu	Asn	Asp	Ala	Thr	Thr	
			20				25						30			
cag	gtg	tcg	cac	atc	ctc	ggc	aat	gcc	ttc	acc	cga	tct	ggg	ctc	aac	144
Gln	Val	Ser	His	Ile	Leu	Gly	Asn	Ala	Phe	Thr	Arg	Ser	Gly	Leu	Asn	
			35				40						45			
gct	gag	tac	gcg	aat	ctt	tat	ggg	cag	gcg	ttg	gtg	ggc	atg	gtg	tcg	192
Ala	Glu	Tyr	Ala	Asn	Leu	Tyr	Gly	Gln	Ala	Leu	Val	Gly	Met	Val	Ser	
			50				55				60					

atg acg gcg caa tgg tgg ttg gat gag cgc act ccg ccg aag gaa gaa 240
 Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65 70 75 80

gtt gcc gca cat att gtt aat ctt tgt tgg aat ggt ttg acg ggg atg 288
 Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
 85 90 95

gaa gcc gat ccg aag tta act ccc atc agt tct gct gag ggt gcg att 336
 Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
 100 105 110

ttt ggt caa gaa aag gag agt gaa gcg tgacacctat gctcgcgggg 383
 Phe Gly Gln Glu Lys Glu Ser Glu Ala
 115 120

ctg 386

<210> 318

<211> 121

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg
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Pro Gly Glu Arg Arg Ser Tyr Gly Thr Leu Leu Asn Asp Ala Thr Thr
 20 25 30

Gln Val Ser His Ile Leu Gly Asn Ala Phe Thr Arg Ser Gly Leu Asn
 35 40 45

Ala Glu Tyr Ala Asn Leu Tyr Gly Gln Ala Leu Val Gly Met Val Ser
 50 55 60

Met Thr Ala Gln Trp Trp Leu Asp Glu Arg Thr Pro Pro Lys Glu Glu
 65 70 75 80

Val Ala Ala His Ile Val Asn Leu Cys Trp Asn Gly Leu Thr Gly Met
 85 90 95

Glu Ala Asp Pro Lys Leu Thr Pro Ile Ser Ser Ala Glu Gly Ala Ile
 100 105 110

Phe Gly Gln Glu Lys Glu Ser Glu Ala
 115 120

<210> 319

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(760)

<223> RXS01082

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cacttatcaa acatcggcgg cgaattaaga aggtgaacag ttg acg cag tgg ggt 115
                                   Leu Thr Gln Trp Gly
                                   1       5

aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa 163
Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu
                        10                        15                        20

gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga 211
Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly
                        25                        30                        35

gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag 259
Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu
                        40                        45                        50

ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca 307
Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala
                        55                        60                        65

ggg cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag 355
Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu
70                        75                        80                        85

acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc 403
Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly
                        90                        95                        100

gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag 451
Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys
105                        110                        115

atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc 499
Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro
120                        125                        130

atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt 547
Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu
135                        140                        145

ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac 595
Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp
150                        155                        160                        165

gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg 643
Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val
170                        175                        180

ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg 691
Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu
185                        190                        195

cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca 739
Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala
200                        205                        210

aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct 783
Asn Ala Val Arg Val Ser Arg

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215

220

<210> 320

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
20 25 30

Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
35 40 45

Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
50 55 60

Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg
65 70 75 80

Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala
85 90 95

His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro
100 105 110

Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp
115 120 125

Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn
130 135 140

Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val
145 150 155 160

Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly
165 170 175

Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser
180 185 190

Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile
195 200 205

Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg
210 215 220

<210> 321

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXS01123

<400> 321

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gtggcggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc 115
                                         Met Arg Thr Leu Ala
                                         1           5

gcg gag cta aat atc aag gcg ccg tgc ctg tac aag cat gta aaa acg 163
Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
                        10                        15                        20

cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg 211
Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
                        25                        30                        35

ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg 259
Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
                        40                        45                        50

gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc 307
Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
                        55                        60                        65

acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act 355
Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
                        70                        75                        80                        85

tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag 403
Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
                        90                        95                        100

ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc 451
Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
                        105                        110                        115

gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg 499
Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
                        120                        125                        130

tgg gag atc ggc gcg cgg gca ttt gac aca caa gta ttc gac caa ggc 547
Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
                        135                        140                        145

tgagcaaaaa ggcgctaagc tgt 570

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<210> 322

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 322

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Met Arg Thr Leu Ala Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr
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Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
      20           25           30

Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
  35           40           45

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Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
 50 55 60
 Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
 65 70 75 80
 Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
 85 90 95
 His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
 100 105 110
 Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
 115 120 125
 Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
 130 135 140
 Val Phe Asp Gln Gly
 145

<210> 323
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(709)
 <223> RXS01189

<400> 323
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 taatgcacct gcaaatacac ctgcagaaaa ggaagcttaa atg att tcc att tcc 115
 Met Ile Ser Ile Ser
 1 5
 atc gcc gac gac gaa gcc ctg atc gca agc tcc ctg gca acc ttg ctc 163
 Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser Leu Ala Thr Leu Leu
 10 15 20
 agc ttg gaa ccc gat tta gac gtc cga cct acc gca gga tcc ggt gaa 211
 Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr Ala Gly Ser Gly Glu
 25 30 35
 gaa ctc att gaa acg tgg gcg gat cca agc aac cga acc gat gta tgc 259
 Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn Arg Thr Asp Val Cys
 40 45 50
 gtc ctt gac ctt caa ctc gga ggc atc gac ggc atc gac acc gcc acc 307
 Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly Ile Asp Thr Ala Thr
 55 60 65
 cgg ctc atg gaa acc acc cca gat ttg gcc gtg ctc atc gtg acc agc 355
 Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val Leu Ile Val Thr Ser
 70 75 80 85
 cac gcc agg ccc cga caa ctc aaa cgc gcg ctt gca gca ggt gtt tta 403

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<210> 324
<211> 203
<212> PRT
<213> Corynebacterium glutamicum
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<400> 324																
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Leu	Ala	Thr	Leu	Leu	Ser	Leu	Glu	Pro	Asp	Leu	Asp	Val	Arg	Pro	Thr	
			20					25					30			
Ala	Gly	Ser	Gly	Glu	Glu	Leu	Ile	Glu	Thr	Trp	Ala	Asp	Pro	Ser	Asn	
		35					40					45				
Arg	Thr	Asp	Val	Cys	Val	Leu	Asp	Leu	Gln	Leu	Gly	Gly	Ile	Asp	Gly	
	50					55					60					
Ile	Asp	Thr	Ala	Thr	Arg	Leu	Met	Glu	Thr	Thr	Pro	Asp	Leu	Ala	Val	
65					70					75					80	
Leu	Ile	Val	Thr	Ser	His	Ala	Arg	Pro	Arg	Gln	Leu	Lys	Arg	Ala	Leu	
				85					90					95		
Ala	Ala	Gly	Val	Leu	Gly	Phe	Leu	Pro	Lys	Thr	Ser	Thr	Ala	Asp	Glu	
			100					105					110			
Phe	Ala	Thr	Ala	Ile	Arg	Thr	Val	His	Ala	Gly	Arg	Arg	Tyr	Ile	Asp	
		115					120					125				

Pro Glu Leu Ala Ala Met Thr Ile Ser Ala Gly Glu Ser Pro Leu Thr
 130 135 140

Asn Arg Glu Glu Glu Val Leu Glu Leu Ala Gly Gln Gly Leu Ser Ala
 145 150 155 160

Glu Glu Ile Ala Val Ala Ala His Leu Ala Pro Gly Thr Thr Arg Asn
 165 170 175

Tyr Leu Ser Gln Ala Met Thr Lys Val Gly Ala Gln Asn Arg Phe Glu
 180 185 190

Ala Phe Thr Arg Ala Arg Glu Leu Gly Trp Leu
 195 200

<210> 325

<211> 900

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> RXS01242

<400> 325

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gacatatatta gtaaattggc tttttgcttt aaggagtgc atg tac gca gag gag 115
 Met Tyr Ala Glu Glu
 1 5

cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163
 Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn
 10 15 20

gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211
 Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg
 25 30 35

cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac 259
 Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His
 40 45 50

ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307
 Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu
 55 60 65

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag 355
 Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
 70 75 80 85

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat 403
 Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
 90 95 100

gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct 451
 Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
 105 110 115

agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt 499
 Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
 120 125 130

aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
 Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
 135 140 145

gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
 Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
 150 155 160 165

ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
 Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
 170 175 180

acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
 Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
 185 190 195

aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
 Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
 200 205 210

tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc 787
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
 215 220 225

gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
 250 255

tgattcttac agtcactgca agt 900

<210> 326
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 326
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 Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
 20 25 30
 Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45
 Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60
 Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80

<400> 327																	
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tttccgccccg ttttccctat ccacaaaagg accaagataa																	
											gtg	atc	cgt	att	ctg		115
											Val	Ile	Arg	Ile	Leu		
											1				5		
ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg																	163
Leu	Ala	Asp	Asp	His	Pro	Val	Val	Arg	Ala	Gly	Leu	Ala	Ser	Leu	Leu		
				10					15					20			
gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat																	211
Val	Ser	Glu	Asp	Asp	Phe	Glu	Ile	Val	Asp	Met	Val	Gly	Thr	Pro	Asp		
			25					30					35				

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259
Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met
40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc ggc ggg gta 307
Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val
55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355
Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu
70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403
Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser
90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451
Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu
105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499
Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys
120 125 130

cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547
Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala
135 140 145

ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595
Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln
150 155 160 165

agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643
Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val
170 175 180

aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691
Lys Ser His Met Gly His Val Phe Asn Lys Leu Asp Val Thr Ser Arg
185 190 195

aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740
Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile
200 205 210

cgtgttggtgta acc 753

<210> 328

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

Val Ile Arg Ile Leu Leu Ala Asp Asp His Pro Val Val Arg Ala Gly
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Leu Ala Ser Leu Leu Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met
20 25 30

Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val

35					40					45					
Asp	Val	Val	Leu	Met	Asp	Leu	Arg	Phe	Gly	Asp	Gln	Pro	Gly	Ile	Glu
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Val	Ala	Gly	Gly	Val	Glu	Ala	Thr	Arg	Arg	Ile	Arg	Ala	Leu	Asp	Asn
65					70					75					80
Pro	Pro	Gln	Val	Leu	Val	Val	Thr	Asn	Tyr	Ser	Thr	Asp	Gly	Asp	Val
				85					90					95	
Val	Gly	Ala	Val	Ser	Ala	Gly	Ala	Val	Gly	Tyr	Leu	Leu	Lys	Asp	Ser
			100					105					110		
Ser	Pro	Glu	Asp	Leu	Ile	Ala	Gly	Val	Arg	Asp	Ala	Ala	Arg	Gly	Glu
		115					120					125			
Ser	Val	Leu	Ser	Lys	Gln	Val	Ala	Ser	Lys	Ile	Met	Gly	Arg	Met	Asn
	130					135					140				
Asn	Pro	Met	Thr	Ala	Leu	Ser	Ala	Arg	Glu	Ile	Glu	Val	Leu	Ser	Leu
145					150					155					160
Val	Ala	Gln	Gly	Gln	Ser	Asn	Arg	Glu	Ile	Gly	Lys	Lys	Leu	Phe	Leu
				165					170					175	
Thr	Glu	Ala	Thr	Val	Lys	Ser	His	Met	Gly	His	Val	Phe	Asn	Lys	Leu
			180					185					190		
Asp	Val	Thr	Ser	Arg	Thr	Ala	Ala	Val	Ala	Glu	Ala	Arg	Gln	Arg	Gly
		195				200						205			
Ile	Ile														
	210														

<210> 329
 <211> 1017
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(994)
 <223> RXS01674

<400> 329
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 cggtagacgg tactttcata tccaccata taatgttgat atg gat aat ggg tgg 115
 Met Asp Asn Gly Trp
 1 5
 ccg aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg 163
 Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly
 10 15 20
 agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc 211
 Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala
 25 30 35

agt	cgg	gct	atc	gca	gag	ctt	gag	gca	gac	atg	aaa	gcc	gaa	ttg	ttg	259
Ser	Arg	Ala	Ile	Ala	Glu	Leu	Glu	Ala	Asp	Met	Lys	Ala	Glu	Leu	Leu	
		40					45					50				
gta	cgt	cat	cct	cga	gga	tca	cat	cca	aca	gct	gct	gga	ctt	gcg	ctt	307
Val	Arg	His	Pro	Arg	Gly	Ser	His	Pro	Thr	Ala	Ala	Gly	Leu	Ala	Leu	
	55					60					65					
gtt	gag	cat	tcg	cgc	gat	ctg	ctt	caa	tct	gta	caa	gaa	ttt	act	gaa	355
Val	Glu	His	Ser	Arg	Asp	Leu	Leu	Gln	Ser	Val	Gln	Glu	Phe	Thr	Glu	
	70				75					80					85	
tgg	gtg	aca	gag	gga	cga	act	gag	cag	cgg	ctg	aaa	ttg	cat	gtt	ggg	403
Trp	Val	Thr	Glu	Gly	Arg	Thr	Glu	Gln	Pro	Leu	Lys	Leu	His	Val	Gly	
				90					95					100		
gcc	agt	atg	acc	att	gcc	gag	gct	cta	ctt	cca	gct	tgg	gtt	gcg	gac	451
Ala	Ser	Met	Thr	Ile	Ala	Glu	Ala	Leu	Leu	Pro	Ala	Trp	Val	Ala	Asp	
			105					110					115			
atg	cgc	acg	cgt	ttt	cct	gcc	tgc	cgt	gtc	gac	gtc	tct	gtg	atg	aat	499
Met	Arg	Thr	Arg	Phe	Pro	Ala	Cys	Arg	Val	Asp	Val	Ser	Val	Met	Asn	
		120					125					130				
tct	tct	caa	gta	att	gaa	gcc	gtc	cag	aaa	ggg	cac	ttg	caa	cta	ggg	547
Ser	Ser	Gln	Val	Ile	Glu	Ala	Val	Gln	Lys	Gly	His	Leu	Gln	Leu	Gly	
	135					140					145					
ttt	att	gaa	aca	ccg	cat	gtt	ccc	gta	cgg	ctt	cat	gct	cgt	gtg	gtg	595
Phe	Ile	Glu	Thr	Pro	His	Val	Pro	Val	Arg	Leu	His	Ala	Arg	Val	Val	
	150				155					160					165	
caa	gag	gac	aag	ctg	att	gtg	gtg	att	tct	cct	aat	cat	gag	tgg	gct	643
Gln	Glu	Asp	Lys	Leu	Ile	Val	Val	Ile	Ser	Pro	Asn	His	Glu	Trp	Ala	
				170					175					180		
aat	cgc	acg	ggg	agg	atc	agt	ctt	cgg	gag	ttg	tcg	gaa	act	ccg	ctg	691
Asn	Arg	Thr	Gly	Arg	Ile	Ser	Leu	Arg	Glu	Leu	Ser	Glu	Thr	Pro	Leu	
			185					190					195			
ata	gtg	agg	gaa	gtc	ggc	tca	ggg	acc	cga	gaa	gca	tta	caa	gaa	tta	739
Ile	Val	Arg	Glu	Val	Gly	Ser	Gly	Thr	Arg	Glu	Ala	Leu	Gln	Glu	Leu	
		200					205					210				
ctt	gcg	gat	tat	gac	atg	gct	gag	cgg	att	caa	gtg	tta	aac	agc	aat	787
Leu	Ala	Asp	Tyr	Asp	Met	Ala	Glu	Pro	Ile	Gln	Val	Leu	Asn	Ser	Asn	
	215					220					225					
gct	gcg	gta	cgt	gtt	gtt	gtt	gaa	gca	ggg	gca	ggg	cct	gca	gta	ctt	835
Ala	Ala	Val	Arg	Val	Val	Val	Glu	Ala	Gly	Ala	Gly	Pro	Ala	Val	Leu	
	230				235					240					245	
ggg	gaa	tta	gcc	ttg	cgt	gat	cat	ctt	gcg	ctc	ggc	agg	ctg	ttg	agt	883
Gly	Glu	Leu	Ala	Leu	Arg	Asp	His	Leu	Ala	Leu	Gly	Arg	Leu	Leu	Ser	
			250						255					260		
gtg	cca	ttt	gaa	ggc	agt	gga	gtt	act	cgt	cct	ctt	aca	gct	gtg	tgg	931
Val	Pro	Phe	Glu	Gly	Ser	Gly	Val	Thr	Arg	Pro	Leu	Thr	Ala	Val	Trp	
			265					270					275			
agt	gga	ccc	cgc	aga	ttg	ccg	att	cta	gcg	gga	gaa	tta	gtg	tcc	atc	979

Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
 280 285 290

gca tcg aac cac atc tgattttgag ccctggctaa cgg
 Ala Ser Asn His Ile
 295

1017

<210> 330

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

Met Asp Asn Gly Trp Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala
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Ile Val Glu Glu Gly Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met
 20 25 30

Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
 35 40 45

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
 50 55 60

Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65 70 75 80

Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
 85 90 95

Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
 100 105 110

Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
 115 120 125

Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
 130 135 140

His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
 145 150 155 160

His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175

Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
 180 185 190

Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
 195 200 205

Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
 210 215 220

Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
 225 230 235 240

Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu
 245 250 255

Gly Arg Leu Leu Ser Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro
 260 265 270

Leu Thr Ala Val Trp Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly
 275 280 285

Glu Leu Val Ser Ile Ala Ser Asn His Ile
 290 295

<210> 331

<211> 928

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXS01872

<400> 331

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tagctgtttt tgattcactt tgtgcatgta ggctgtgacc atg ggc aac gac ggc 115
 Met Gly Asn Asp Gly
 1 5

gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163
 Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
 10 15 20

tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211
 Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
 25 30 35

aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
 Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
 40 45 50

ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac 307
 Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
 55 60 65

gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355
 Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala
 70 75 80 85

gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403
 Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg
 90 95 100

ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc 451
 Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
 105 110 115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499
 Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln
 120 125 130

gcg gca gca atg ctc ctg gta gat cgt gtt ttg gct gat gaa act gac , 547

Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu Ala Asp Glu Thr Asp
 135 140 145

ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg 595
 Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly
 150 155 160 165

tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat 643
 Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp
 170 175 180

cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act 691
 His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr
 185 190 195

gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc ggc acc cga 739
 Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg
 200 205 210

ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg 787
 Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val
 215 220 225

gtt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca 835
 Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala Gly Leu Val Ser Ala
 230 235 240 245

ggt ctc ggc gtt ggt gtg gtt ccg atg gat gat ccc tac ctt tcc aca 883
 Gly Leu Gly Val Gly Val Val Pro Met Asp Asp Pro Tyr Leu Ser Thr
 250 255 260

gtg gga atc gtg caa cgc cca ctt agt cca ccc gct tat agg gaa 928
 Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro Ala Tyr Arg Glu
 265 270 275

<210> 332

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
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Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
 35 40 45

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
 50 55 60

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
 65 70 75 80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
 85 90 95

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met

100	105	110
Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu		
115	120	125
Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu		
130	135	140
Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val		
145	150	155
Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu		
165	170	175
Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu		
180	185	190
Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala		
195	200	205
Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly		
210	215	220
Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala		
225	230	235
Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp		
245	250	255
Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro		
260	265	270
Ala Tyr Arg Glu		
275		

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 Val Ser Thr Asp Pro
 1 5
 gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc 163
 Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile
 10 15 20
 atc ctg ctc acc cgg tat ggt gtc caa aac aca ccg acc aac aag cgc 211
 Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg
 25 30 35

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<400> 334
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Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu
          35          40          45
Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala
  50          55          60
Glu Ser Phe Gly Leu Asn Val Ser Thr Val His Arg Gln Leu Lys Ala
  65          70          75          80
Ala Ile Ala Asn Gly Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro
          85          90          95
Ala Lys Leu His Arg Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln
          100          105          110
Glu Leu Leu Ala Arg Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp

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115	120	125
Asp Glu Glu Asp Ile Lys Thr His Ala Lys Leu Leu Arg Lys His Asn		
130	135	140
Glu Ser Leu Glu Glu Tyr Leu Asp Met Lys Trp Pro Arg Pro		
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 <223> RXS02288

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agtgcctggat ctaacaacat ttccgtggta actttttcac atg tcc caa gtg att 115
 Met Ser Gln Val Ile
 1 5

ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163
 Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
 10 15 20

acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211
 Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
 25 30 35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac 259
 Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp
 40 45 50

aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg 307
 Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser
 55 60 65

atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt 355
 Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val
 70 75 80 85

aaa gag gcg ttg tgt act gca gca gca cgg ttg att ccg gag ggc gct 403
 Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala
 90 95 100

gtg gtg gcg att gat gat tcc acc acg ttg gag tct ttg gtt gag aag 451
 Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys
 105 110 115

ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca 499
 Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr
 120 125 130

atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att 547
 Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile
 135 140 145

gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag 595
 Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys
 150 155 160 165

gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt 643
 Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val
 170 175 180

tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat 691
 Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His
 185 190 195

cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt 739
 Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly
 200 205 210

agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt 787
 Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly
 215 220 225

gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat 835
 Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp
 230 235 240 245

cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg 883
 Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala
 250 255 260

cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca 931
 Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
 265 270 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa 969
 Thr Glu Glu Asp Phe
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<210> 336

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

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Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
 35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
 50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
 65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
 100 105 110
 Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
 115 120 125
 His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
 130 135 140
 Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
 145 150 155 160
 Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
 165 170 175
 Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
 180 185 190
 Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
 195 200 205
 Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
 210 215 220
 Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
 225 230 235 240
 His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
 245 250 255
 Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
 260 265 270
 Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
 275 280

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 <211> 567
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(544)
 <223> RXS02573

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 gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc 115
 Met Thr Asn Lys Thr
 1 5
 atg ctg gtt gct ttt gat ggc tca ccg gaa tcc cgg cgc gct ttg gaa 163
 Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu
 10 15 20
 tat gcg gcg aaa ttg ttg cag ccg cgc acc gtg gaa att tta act gcg 211
 Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala

25										30					35					
tgg	gag	cca	ttg	cat	cgg	caa	gct	gcg	cgc	tcg	gtt	tcg	ttg	atc	acc	259				
Trp	Glu	Pro	Leu	His	Arg	Gln	Ala	Ala	Arg	Ser	Val	Ser	Leu	Ile	Thr					
	40						45					50								
ttg	ggg	gtg	gaa	ccc	gaa	gac	ccc	gcc	cat	tcc	gct	gca	cta	aaa	acc	307				
Leu	Gly	Val	Glu	Pro	Glu	Asp	Pro	Ala	His	Ser	Ala	Ala	Leu	Lys	Thr					
	55					60					65									
tgc	cag	gaa	ggc	gta	gag	cta	gcc	caa	tct	cta	ggt	ctg	gaa	gcg	cga	355				
Cys	Gln	Glu	Gly	Val	Glu	Leu	Ala	Gln	Ser	Leu	Gly	Leu	Glu	Ala	Arg					
	70				75					80					85					
gcc	cac	atg	gtg	gaa	tcc	gca	acg	gcc	gtg	tgg	agc	gcc	atc	gtt	gat	403				
Ala	His	Met	Val	Glu	Ser	Ala	Thr	Ala	Val	Trp	Ser	Ala	Ile	Val	Asp					
				90					95					100						
gct	gct	gac	gag	ctc	cgc	ccc	gac	gtg	att	gtc	acc	ggc	acc	cgc	ggg	451				
Ala	Ala	Asp	Glu	Leu	Arg	Pro	Asp	Val	Ile	Val	Thr	Gly	Thr	Arg	Gly					
			105					110					115							
atc	tcc	gga	tgg	aaa	tcc	ctg	tgg	caa	tcc	tcc	acc	tca	gac	agc	gtg	499				
Ile	Ser	Gly	Trp	Lys	Ser	Leu	Trp	Gln	Ser	Ser	Thr	Ser	Asp	Ser	Val					
	120						125					130								
ctc	cac	cac	gcc	gac	gta	cca	gtt	ttt	gtc	gtt	cca	ccc	ctg	gac		544				
Leu	His	His	Ala	Asp	Val	Pro	Val	Phe	Val	Val	Pro	Pro	Leu	Asp						
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<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

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Arg	Arg	Ala	Leu	Glu	Tyr	Ala	Ala	Lys	Leu	Leu	Gln	Pro	Arg	Thr	Val
		20						25					30		

Glu	Ile	Leu	Thr	Ala	Trp	Glu	Pro	Leu	His	Arg	Gln	Ala	Ala	Arg	Ser
	35					40						45			

Val	Ser	Leu	Ile	Thr	Leu	Gly	Val	Glu	Pro	Glu	Asp	Pro	Ala	His	Ser
	50					55					60				

Ala	Ala	Leu	Lys	Thr	Cys	Gln	Glu	Gly	Val	Glu	Leu	Ala	Gln	Ser	Leu
65					70					75					80

Gly	Leu	Glu	Ala	Arg	Ala	His	Met	Val	Glu	Ser	Ala	Thr	Ala	Val	Trp
			85						90					95	

Ser	Ala	Ile	Val	Asp	Ala	Ala	Asp	Glu	Leu	Arg	Pro	Asp	Val	Ile	Val
		100						105					110		

Thr	Gly	Thr	Arg	Gly	Ile	Ser	Gly	Trp	Lys	Ser	Leu	Trp	Gln	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125	
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130	135	140	
Pro Pro Leu Asp			
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gga gat gct gag gct gcg ctg gaa ttc ggt gtg cag cct gtg ggt gca	96		
Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala			
20 25 30			
tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag	144		
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu			
35 40 45			
gat tct gcc tac gat gaa gcg cca gaa ata atc gga acc atg gaa ccg	192		
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro			
50 55 60			
gag tat gaa aag att gca gcg ctt gaa ccg gat ctg att ttg gac gtg	240		
Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val			
65 70 75 80			
cgc agc tct ggc gac cag gaa cgc tat gac aag ttg tct tca atc gca	288		
Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala			
85 90 95			
ctg acc atc ggc gtt cca gaa ggt ggc gat agc tac ctc acc cca cgc	336		
Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg			
100 105 110			
gct gag cag gta acc atg atc gcc act gct ctg ggg cag gct gaa cgt	384		
Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg			
115 120 125			
ggt gaa gaa gtg aac gct gaa tac gag cag ctc act gct gat att cgt	432		
Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg			
130 135 140			
gca gct cac ccg ggc tgg cct gag aag acc gcg gct gct gta tct gca	480		
Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Ala Val Ser Ala			
145 150 155 160			
acg gca acc agc tgg ggt gca tac atc aag ggc tcc aac cgt gta gat	528		

Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
 165 170 175
 act ttg ctg gac ctg ggc ttc cag gaa aac cct gag ctg gct aaa cag 576
 Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
 180 185 190
 caa cct ggc gat acg ggt ttc tcc atc aaa ttc agt gaa gag act ttc 624
 Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
 195 200 205
 ggc gtt gtg gat tcc gac ctg gtt gtc ggc ttt gcc atc ggt atg act 672
 Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
 210 215 220
 cct gag gaa atg gca gag cag gtt cca tgg cag atg ttg acc gcc act 720
 Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
 225 230 235 240
 cgt gac ggc cgt tcc ttt gtg atg ccc cgt gag att tcc aat gcg ttt 768
 Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
 245 250 255
 tct ttg ggt tcc ccg cag tcc act cgg ttc gcg tta gac gcc ttg gtg 816
 Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
 260 265 270
 cca ctt ctg gag gag cat gca ggg gag tagtggtccg gtggtgcggg cag 866
 Pro Leu Leu Glu Glu His Ala Gly Glu
 275 280

<210> 340

<211> 281

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

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 20 25 30
 Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
 35 40 45
 Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
 50 55 60
 Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
 65 70 75 80
 Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
 85 90 95
 Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
 100 105 110
 Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg

115					120					125					
Gly	Glu	Glu	Val	Asn	Ala	Glu	Tyr	Glu	Gln	Leu	Thr	Ala	Asp	Ile	Arg
130						135					140				
Ala	Ala	His	Pro	Gly	Trp	Pro	Glu	Lys	Thr	Ala	Ala	Ala	Val	Ser	Ala
145					150					155					160
Thr	Ala	Thr	Ser	Trp	Gly	Ala	Tyr	Ile	Lys	Gly	Ser	Asn	Arg	Val	Asp
				165					170					175	
Thr	Leu	Leu	Asp	Leu	Gly	Phe	Gln	Glu	Asn	Pro	Glu	Leu	Ala	Lys	Gln
			180					185					190		
Gln	Pro	Gly	Asp	Thr	Gly	Phe	Ser	Ile	Lys	Phe	Ser	Glu	Glu	Thr	Phe
		195					200					205			
Gly	Val	Val	Asp	Ser	Asp	Leu	Val	Val	Gly	Phe	Ala	Ile	Gly	Met	Thr
210						215					220				
Pro	Glu	Glu	Met	Ala	Glu	Gln	Val	Pro	Trp	Gln	Met	Leu	Thr	Ala	Thr
225					230					235					240
Arg	Asp	Gly	Arg	Ser	Phe	Val	Met	Pro	Arg	Glu	Ile	Ser	Asn	Ala	Phe
				245					250					255	
Ser	Leu	Gly	Ser	Pro	Gln	Ser	Thr	Arg	Phe	Ala	Leu	Asp	Ala	Leu	Val
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Pro	Leu	Leu	Glu	Glu	His	Ala	Gly	Glu							
		275					280								

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 <212> DNA
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 <222> (101)..(907)
 <223> RXS02691

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 Met Asn Thr Met Pro
 1 5
 gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg 163
 Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val
 10 15 20
 gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca 211
 Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro
 25 30 35
 aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag 259
 Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln
 40 45 50

ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag 307
 Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys
 55 60 65

tat ggc gtc agc cga att acg gtt cgt cgg gcg att ggt gat ctg gtc 355
 Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val
 70 75 80 85

gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc 403
 Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala
 90 95 100

cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag 451
 His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu
 105 110 115

atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc 499
 Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser
 120 125 130

cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc 547
 Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg
 135 140 145

gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga 595
 Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg
 150 155 160 165

ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac 643
 Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp
 170 175 180

ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc 691
 Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg
 185 190 195

gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta 739
 Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val
 200 205 210

gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc 787
 Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala
 215 220 225

cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg 835
 Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val
 230 235 240 245

gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca 883
 Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr
 250 255 260

ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggt ggc 930
 Leu Val Thr Arg Ser Glu Asp Leu
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<210> 342

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

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 Ala Ser Lys Gly Val Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val
 20 25 30
 Asp Gly Leu Lys Pro Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu
 35 40 45
 Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg
 50 55 60
 Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala
 65 70 75 80
 Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys
 85 90 95
 Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala
 100 105 110
 Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg
 115 120 125
 Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe
 130 135 140
 Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg
 145 150 155 160
 Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser
 165 170 175
 Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr
 180 185 190
 Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln
 195 200 205
 Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp
 210 215 220
 Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser
 225 230 235 240
 Gly Asp Lys Pro Val Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg
 245 250 255
 Tyr Ser Leu Lys Thr Leu Val Thr Arg Ser Glu Asp Leu
 260 265

<210> 343

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(1138)
 <223> RXS02730

<400> 343

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ccaacatcgc cttgcacgta ataggttaaa acacaagtga atgtaatcgt ttgcagcaat 60

cgattacata aaggtagata atgagataaaa gcgaggcgct atg gcg acg gaa aaa 115
                                         Met Ala Thr Glu Lys
                                         1                               5

ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163
Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
                        10                        15                        20

gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211
Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
                        25                        30                        35

act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259
Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala
                        40                        45                        50

aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt 307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly
                        55                        60                        65

gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act 355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr
                        70                        75                        80                        85

gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc 403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr
                        90                        95                        100

aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc 451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu
                        105                        110                        115

acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc 499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys
                        120                        125                        130

gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg 547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu
                        135                        140                        145

gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct 595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser
                        150                        155                        160                        165

aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac 643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn
                        170                        175                        180

aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca 691
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr
                        185                        190                        195

ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa 739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys

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200	205	210	
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ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe 230 235 240 245			835
gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys 250 255 260			883
gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr 265 270 275			931
cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln 280 285 290			979
aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu 295 300 305			1027
att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala 310 315 320 325			1075
ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp 330 335 340			1123
gga ctc ccc aat gag taactcaacc ggtaccgaca ttg Gly Leu Pro Asn Glu 345			1161

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<212> PRT

<213> Corynebacterium glutamicum

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Ala	Gly	Val	Ser	Ile	Ala	Thr	Ala	Ser	Arg	Ala	Leu	Ala	Asp	Asn	Pro
			20					25					30		

Ala	Val	Ala	Ala	Ser	Thr	Arg	Glu	Arg	Ile	Gln	Gln	Leu	Ala	Ser	Asp
		35					40					45			

Leu	Gly	Tyr	Arg	Ala	Asn	Ala	Gln	Ala	Arg	Ala	Leu	Arg	Ser	Ser	Arg
	50				55						60				

Ser	Asn	Thr	Ile	Gly	Val	Ile	Val	Pro	Ser	Leu	Ile	Asn	His	Tyr	Phe
65					70					75					80

Ala	Ala	Met	Val	Thr	Glu	Ile	Gln	Ser	Thr	Ala	Ser	Lys	Ala	Gly	Leu
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Ser	Tyr	Ser	Arg	Lys	Phe	Leu	Thr	Gln	Val	Trp	Ile	Arg	Asp	Asn	Val	
1				5					10					15		
ggc	gat	tat	aaa	ggc	ctt	acc	gat	acg	gcg	ttc	cgt	aag	aag	ctg	cag	96
Gly	Asp	Tyr	Lys	Gly	Leu	Thr	Asp	Thr	Ala	Phe	Arg	Lys	Lys	Leu	Gln	
			20					25					30			
cgc	gat	ctt	gcc	tac	ctg	cgc	aga	ggt	ggc	ggt	ccg	att	gag	cag	ttc	144
Arg	Asp	Leu	Ala	Tyr	Leu	Arg	Arg	Val	Gly	Val	Pro	Ile	Glu	Gln	Phe	
		35					40					45				
acg	gtc	acc	tca	ggc	ata	gct	gaa	ggc	cag	cag	gcg	tac	cgt	ctg	gcc	192
Thr	Val	Thr	Ser	Gly	Ile	Ala	Glu	Gly	Gln	Gln	Ala	Tyr	Arg	Leu	Ala	
	50					55					60					
cag	gat	tct	tat	aag	ctc	ccc	gag	gtc	gaa	ttc	acc	cca	gat	gag	gcc	240
Gln	Asp	Ser	Tyr	Lys	Leu	Pro	Glu	Val	Glu	Phe	Thr	Pro	Asp	Glu	Ala	
65					70					75					80	
gcc	gtg	ctg	ggc	atg	gca	ggg	gag	atg	ggc	cat	aat	cag	gaa	ctc	ggc	288
Ala	Val	Leu	Gly	Met	Ala	Gly	Glu	Met	Gly	His	Asn	Gln	Glu	Leu	Gly	
				85					90					95		
gcc	ttc	gcg	cgt	tcg	ggg	tgg	acc	aaa	ttg	gcg	gcc	ggc	ggc	gcg	cag	336
Ala	Phe	Ala	Arg	Ser	Gly	Trp	Thr	Lys	Leu	Ala	Ala	Gly	Gly	Ala	Gln	
			100					105					110			
cgt	gat	ctg	tcc	acg	tcc	aca	gcc	ttg	acc	aat	gcg	ggc	gat	tta	ggc	384
Arg	Asp	Leu	Ser	Thr	Ser	Thr	Ala	Leu	Thr	Asn	Ala	Gly	Asp	Leu	Gly	
		115					120					125				
tcc	ttg	tct	gca	aaa	acc	ctc	gat	gcg	atc	atc	aaa	gcc	cgc	caa	ttg	432
Ser	Leu	Ser	Ala	Lys	Thr	Leu	Asp	Ala	Ile	Ile	Lys	Ala	Arg	Gln	Leu	
	130					135					140					
ggc	aag	caa	atc	agc	ttc	gaa	tac	cgg	cgc	gcc	ccc	aaa	gac	gcc	ccc	480
Gly	Lys	Gln	Ile	Ser	Phe	Glu	Tyr	Arg	Arg	Ala	Pro	Lys	Asp	Ala	Pro	
145					150					155					160	
tcg	ctt	cga	cac	atg	gat	cct	tgg	ggc	ctg	gtc	cct	gag	cgc	gac	cgc	528
Ser	Leu	Arg	His	Met	Asp	Pro	Trp	Gly	Leu	Val	Pro	Glu	Arg	Asp	Arg	
				165					170					175		
atc	tac	ctg	gtc	gga	ttc	gac	ctc	gac	cgc	caa	gaa	gca	cgc	acc	ttc	576
Ile	Tyr	Leu	Val	Gly	Phe	Asp	Leu	Asp	Arg	Gln	Glu	Ala	Arg	Thr	Phe	
			180					185					190			
cgc	atc	acc	cgc	gtc	cgc	aac	atc	aaa	ctc							606
Arg	Ile	Thr	Arg	Val	Arg	Asn	Ile	Lys	Leu							
		195				200										

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<212> PRT

<213> Corynebacterium glutamicum

<400> 346

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Arg Asp Leu Ala Tyr Leu Arg Arg Val Gly Val Pro Ile Glu Gln Phe	35	40	45
Thr Val Thr Ser Gly Ile Ala Glu Gly Gln Gln Ala Tyr Arg Leu Ala	50	55	60
Gln Asp Ser Tyr Lys Leu Pro Glu Val Glu Phe Thr Pro Asp Glu Ala	65	70	75
Ala Val Leu Gly Met Ala Gly Glu Met Gly His Asn Gln Glu Leu Gly	85	90	95
Ala Phe Ala Arg Ser Gly Trp Thr Lys Leu Ala Ala Gly Gly Ala Gln	100	105	110
Arg Asp Leu Ser Thr Ser Thr Ala Leu Thr Asn Ala Gly Asp Leu Gly	115	120	125
Ser Leu Ser Ala Lys Thr Leu Asp Ala Ile Ile Lys Ala Arg Gln Leu	130	135	140
Gly Lys Gln Ile Ser Phe Glu Tyr Arg Arg Ala Pro Lys Asp Ala Pro	145	150	155
Ser Leu Arg His Met Asp Pro Trp Gly Leu Val Pro Glu Arg Asp Arg	165	170	175
Ile Tyr Leu Val Gly Phe Asp Leu Asp Arg Gln Glu Ala Arg Thr Phe	180	185	190
Arg Ile Thr Arg Val Arg Asn Ile Lys Leu	195	200	

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<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

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agcagttacc ttttccgcgg aaatccgaag ggagccaata atg cgc act agt aaa	115
Met Arg Thr Ser Lys	
1 5	

aaa gag atg att ctg cgc acg gcc atc gat tat atc ggc gag tac agc	163
Lys Glu Met Ile Leu Arg Thr Ala Ile Asp Tyr Ile Gly Glu Tyr Ser	
10 15 20	

ctc gag acg ctg agt tac gat tcg ctc gcc gag gcg acc ggt ctg tcc 211

Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu Ala Thr Gly Leu Ser
 25 30 35
 aag tcg ggc ttg att tat cat ttc ccc agc cgc cat gcg ctg ctt tta 259
 Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg His Ala Leu Leu Leu
 40 45 50
 ggc atg cac gag ttg ctt gcc gac gac tgg gac aag gaa ttg cgc gac 307
 Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp Lys Glu Leu Arg Asp
 55 60 65
 ata acc cgc gac cca gag gat cca ctt gag cga ttg cgc gcc gtc gtg 355
 Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg Leu Arg Ala Val Val
 70 75 80 85
 gtt acg ctt gct gaa aac gtt tcg cgc ccc gag ctg gtt ttg ctt atg 403
 Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu Leu Val Leu Leu Met
 90 95 100
 gac gcc ccc tcc cac ccg gga ttt ctt aac gcc tgg cgc act gta aat 451
 Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala Trp Arg Thr Val Asn
 105 110 115
 cat caa tgg atc ccc gac acc gat gat ctg gaa aac gat gcc cac aaa 499
 His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu Asn Asp Ala His Lys
 120 125 130
 cgc gcc gtc tac tct ggt gca gct cgc agc cga tgg cct ctt cgt gca 547
 Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg Trp Pro Leu Arg Ala
 135 140 145
 cga tta cat tca tgatgatgtc ctcagcaagt cca 582
 Arg Leu His Ser
 150

<210> 348

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

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 Ile Gly Glu Tyr Ser Leu Glu Thr Leu Ser Tyr Asp Ser Leu Ala Glu
 20 25 30
 Ala Thr Gly Leu Ser Lys Ser Gly Leu Ile Tyr His Phe Pro Ser Arg
 35 40 45
 His Ala Leu Leu Leu Gly Met His Glu Leu Leu Ala Asp Asp Trp Asp
 50 55 60
 Lys Glu Leu Arg Asp Ile Thr Arg Asp Pro Glu Asp Pro Leu Glu Arg
 65 70 75 80
 Leu Arg Ala Val Val Val Thr Leu Ala Glu Asn Val Ser Arg Pro Glu
 85 90 95
 Leu Val Leu Leu Met Asp Ala Pro Ser His Pro Gly Phe Leu Asn Ala

100	105	110
Trp Arg Thr Val Asn His Gln Trp Ile Pro Asp Thr Asp Asp Leu Glu		
115	120	125
Asn Asp Ala His Lys Arg Ala Val Tyr Ser Gly Ala Ala Arg Ser Arg		
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Trp Pro Leu Arg Ala Arg Leu His Ser		
145	150	

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 <223> RXS03066

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 Met Thr Ser Asp Lys
 1 5
 gac act gaa caa ttg gaa gcg gca ggc act gaa att tta atg cct cgc 163
 Asp Thr Glu Gln Leu Glu Ala Ala Gly Thr Glu Ile Leu Met Pro Arg
 10 15 20
 cgc cgt ccg gca cag cag cgc agt cgt gaa cga ttc aat cga atc ctc 211
 Arg Arg Pro Ala Gln Gln Arg Ser Arg Glu Arg Phe Asn Arg Ile Leu
 25 30 35
 acc gct gcg cgt tca gtg ctt gtc gat cta ggt ttt gaa tcg ttc acg 259
 Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly Phe Glu Ser Phe Thr
 40 45 50
 ttt gat gaa gtc gct aag cgt gca gag gta ccg atc ggc acg ctg tac 307
 Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro Ile Gly Thr Leu Tyr
 55 60 65
 caa ttc ttt gcc aat aag tat gta ttg atc tgc gaa ttg gat cgt gtg 355
 Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys Glu Leu Asp Arg Val
 70 75 80 85
 gat acc gca gaa gct gtc gcg gag ttg aag aaa ttc tcc gat cag gtt 403
 Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys Phe Ser Asp Gln Val
 90 95 100
 cct gcg ttg cag tgg ccg gat atc ctt gat gaa ttc att gag cac ttg 451
 Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu Phe Ile Glu His Leu
 105 110 115
 gct agg ctc tgg cgc gat gat ccg tct cgg cgg gcc gtg tgg cat gcc 499
 Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg Ala Val Trp His Ala
 120 125 130

atc cag tcc acg ccg gca act cgt gcg aca gct gcg gcg acg gaa aaa 547
 Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala Ala Ala Thr Glu Lys
 135 140 145

gag atg ctg gaa atc atc gcg gaa gtt atg cgc ccg ctt gcc cgc ggt 595
 Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg Pro Leu Ala Arg Gly
 150 155 160 165

gcc ggc tac gag gag cgc atg tca ctg gcg gga ttg ctg gtg cac acg 643
 Ala Gly Tyr Glu Glu Arg Met Ser Leu Ala Gly Leu Leu Val His Thr
 170 175 180

gta agt tcc ctg ctt aac tat gcc gtg cgt gat gtc aat agt tcc gaa 691
 Val Ser Ser Leu Leu Asn Tyr Ala Val Arg Asp Val Asn Ser Ser Glu
 185 190 195

gag gat ttc gac agc atc gtg gaa gaa ata aaa cga atg ctg att tct 739
 Glu Asp Phe Asp Ser Ile Val Glu Glu Ile Lys Arg Met Leu Ile Ser
 200 205 210

tac ctc ttc tcc gtg gct act gga tagtcaacac gcacgttcca ccg 786
 Tyr Leu Phe Ser Val Ala Thr Gly
 215 220

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<211> 221

<212> PRT

<213> Corynebacterium glutamicum

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 20 25 30

Phe Asn Arg Ile Leu Thr Ala Ala Arg Ser Val Leu Val Asp Leu Gly
 35 40 45

Phe Glu Ser Phe Thr Phe Asp Glu Val Ala Lys Arg Ala Glu Val Pro
 50 55 60

Ile Gly Thr Leu Tyr Gln Phe Phe Ala Asn Lys Tyr Val Leu Ile Cys
 65 70 75 80

Glu Leu Asp Arg Val Asp Thr Ala Glu Ala Val Ala Glu Leu Lys Lys
 85 90 95

Phe Ser Asp Gln Val Pro Ala Leu Gln Trp Pro Asp Ile Leu Asp Glu
 100 105 110

Phe Ile Glu His Leu Ala Arg Leu Trp Arg Asp Asp Pro Ser Arg Arg
 115 120 125

Ala Val Trp His Ala Ile Gln Ser Thr Pro Ala Thr Arg Ala Thr Ala
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Ala Ala Thr Glu Lys Glu Met Leu Glu Ile Ile Ala Glu Val Met Arg
 145 150 155 160

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gcataaattg agtttgga aaacaaggaag gcagcctcct																115
Val Lys Asp Leu Val																5
gat acc acc gaa atg tat ctg cgc act att tac gag ctg gaa gaa gag																163
Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr Glu Leu Glu Glu Glu																20
ggc att gtt cct ctg cgt gct cgt atc gca gaa cgc ctt gag cag tcc																211
Gly Ile Val Pro Leu Arg Ala Arg Ile Ala Glu Arg Leu Glu Gln Ser																35
ggc cca act gtc agc cag act gtc gcc cgt atg gaa cgc gac ggt ctt																259
Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu																50
gtg cac gtc agc ccc gac cgc agc ctc gaa atg act cca gag gga cgt																307
Val His Val Ser Pro Asp Arg Ser Leu Glu Met Thr Pro Glu Gly Arg																65
tcc ctc gcc atc gcc gtg atg cgt aag cac cgc cta gca gaa cgc ctc																355
Ser Leu Ala Ile Ala Val Met Arg Lys His Arg Leu Ala Glu Arg Leu																85
ctt acc gac atc atc ggc ttg gac atc cac aaa gtc cac gac gaa gca																403
Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys Val His Asp Glu Ala																100
tgc cgc tgg gag cac gtg atg agt gat gag gtt gaa cgt cgc ctc gtt																451
Cys Arg Trp Glu His Val Met Ser Asp Glu Val Glu Arg Arg Leu Val																115
gaa gtt ctt gac gat gtg cat cgc tcc cct ttc ggt aac cca att cct																499
Glu Val Leu Asp Asp Val His Arg Ser Pro Phe Gly Asn Pro Ile Pro																120
																125
																130

ggc ctc ggc gaa atc ggt ttg gat caa gca gat gag cct gat tcc ggc 547
 Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp Glu Pro Asp Ser Gly
 135 140 145

gtt cgt gcc atc gat ctg 565
 Val Arg Ala Ile Asp Leu
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<210> 352

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Val Lys Asp Leu Val Asp Thr Thr Glu Met Tyr Leu Arg Thr Ile Tyr
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 20 25 30

Arg Leu Glu Gln Ser Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met
 35 40 45

Glu Arg Asp Gly Leu Val His Val Ser Pro Asp Arg Ser Leu Glu Met
 50 55 60

Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg
 65 70 75 80

Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys
 85 90 95

Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val
 100 105 110

Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe
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Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp
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Glu Pro Asp Ser Gly Val Arg Ala Ile Asp Leu
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(562)

<223> FRXA00307

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Glu	Leu	Glu	Glu	Glu	Gly	Ile	Val	Pro	Leu	Arg	Ala	Arg	Ile	Ala	Glu
			20					25					30		
Arg	Leu	Glu	Gln	Ser	Gly	Pro	Thr	Val	Ser	Gln	Thr	Val	Ala	Arg	Met
		35					40					45			
Glu	Arg	Asp	Gly	Leu	Val	His	Val	Ser	Pro	Asp	Arg	Ser	Leu	Glu	Met
	50					55					60				

Thr Pro Glu Gly Arg Ser Leu Ala Ile Ala Val Met Arg Lys His Arg
 65 70 75 80

Leu Ala Glu Arg Leu Leu Thr Asp Ile Ile Gly Leu Asp Ile His Lys
 85 90 95

Val His Asp Glu Ala Cys Arg Trp Glu His Val Met Ser Asp Glu Val
 100 105 110

Glu Arg Arg Leu Val Glu Val Leu Asp Asp Val His Arg Ser Pro Phe
 115 120 125

Gly Asn Pro Ile Pro Gly Leu Gly Glu Ile Gly Leu Asp Gln Ala Asp
 130 135 140

Glu Pro Asp Ser Gly Val Arg Ala Ile Asp
 145 150

<210> 355
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1084)
 <223> RXS03219

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cataatttttt accccaacgc ataggcttaa cggtgtgaat gtg aag tta act gac 115
 Val Lys Leu Thr Asp
 1 5

gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att 163
 Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile
 10 15 20

tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc 211
 Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala
 25 30 35

gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt 259
 Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu
 40 45 50

agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc 307
 Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile
 55 60 65

aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac 355
 Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp
 70 75 80 85

aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa 403
 Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu
 90 95 100

aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca	451
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala	
105 110 115	
gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc	499
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe	
120 125 130	
aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg	547
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val	
135 140 145	
acc agc gat gat gcc act ggt ttg aag gaa ctt gct ctt cat att ttg	595
Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu Ala Leu His Ile Leu	
150 155 160 165	
gat cag gga tac cga gat ata ggt atc att gtc ggt cct gct gag ctc	643
Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val Gly Pro Ala Glu Leu	
170 175 180	
agc acc gcc cga gac cgc aaa gcc gga ttc atc aac gcc ctc gaa acc	691
Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile Asn Ala Leu Glu Thr	
185 190 195	
gaa gcc aca caa cgc gga atc cgc gaa gaa cta cga ttc cgg gta gtt	739
Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu Arg Phe Arg Val Val	
200 205 210	
cac tcc cgc tac tcc ccc acc ggc ggt tat gaa gca ttc gca gaa ttc	787
His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu Ala Phe Ala Glu Phe	
215 220 225	
cgc aat gat ctc cct caa atc gtg gtg ccc ctg agc acg caa tta act	835
Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu Ser Thr Gln Leu Thr	
230 235 240 245	
cta gga gtt ctc aaa gca acc caa gaa aac ggc ata aaa ata tcg gat	883
Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly Ile Lys Ile Ser Asp	
250 255 260	
gac ctg tca ctt gct tgt tac ggc gtc gcc gaa tgg ctc gca gtg tgg	931
Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu Trp Leu Ala Val Trp	
265 270 275	
ggc cct ggc atc acc gtt ttc gca cca gac ctc cca gcc atg ggc gcc	979
Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu Pro Ala Met Gly Ala	
280 285 290	
gca gct gcc acg cag gtt tta acg ctt ctc gac gcc gcc cca ctc ccc	1027
Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp Ala Ala Pro Leu Pro	
295 300 305	
gaa aac cac tta agc att ccg ggg cag ctc att gtc cgt ggg aca act	1075
Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile Val Arg Gly Thr Thr	
310 315 320 325	
cca aag gtt taaaggtaga ggcgacacaat aatgaaaatt	1114
Pro Lys Val	

<210> 356
 <211> 328
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 356
 Val Lys Leu Thr Asp Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr
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 Ala Ser Arg Ala Ile Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg
 20 25 30
 Asp Lys Val Leu Ala Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala
 35 40 45
 Met Ala Arg Ala Leu Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile
 50 55 60
 Val Pro Gly Ile Ile Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu
 65 70 75 80
 Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr
 85 90 95
 Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn
 100 105 110
 Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys
 115 120 125
 Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu
 130 135 140
 Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu
 145 150 155 160
 Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val
 165 170 175
 Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
 180 185 190
 Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu
 195 200 205
 Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu
 210 215 220
 Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu
 225 230 235 240
 Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly
 245 250 255
 Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu
 260 265 270
 Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu
 275 280 285
 Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp

290	295	300	
Ala Ala Pro Leu Pro	Glu Asn His Leu Ser	Ile Pro Gly Gln Leu Ile	
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Val Arg Gly Thr Thr	Pro Lys Val		
	325		
<210> 357			
<211> 1107			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1084)			
<223> FRXA02763			
<400> 357			
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cataatttttt accccaacgc ataggcttaa cggtgtgaat gtg aag tta act gac 115			
		Val Lys Leu Thr Asp	5
		1	
gcc gcc cgt gaa gct gga gta ggt tac ggt act gct tct cgc gca att 163			
Ala Ala Arg Glu Ala Gly Val Gly Tyr Gly Thr Ala Ser Arg Ala Ile			
	10	15	20
tct gga cga ggt tcc gtt gat gca gca acc cgt gac aaa gta ctc gcc 211			
Ser Gly Arg Gly Ser Val Asp Ala Ala Thr Arg Asp Lys Val Leu Ala			
	25	30	35
gcc gcc gag aaa ctt ggg tac cga acc aac gcc atg gct cgt gca ctt 259			
Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala Met Ala Arg Ala Leu			
	40	45	50
agg gaa aac aag acc cgc acc gtt ggc ctg atc gtt ccc ggc att atc 307			
Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile Val Pro Gly Ile Ile			
	55	60	65
aat aag ttc tac acc gaa tcc gcc act gtc ctc caa gat gaa tta gac 355			
Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu Gln Asp Glu Leu Asp			
	70	75	80
aaa tcc gga tac caa cta gtt gtt tcc aca act gga aac gac gca gaa 403			
Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr Gly Asn Asp Ala Glu			
	90	95	100
aag gaa cgt cga gct atc gaa tcc atg ctc aac cgc cag gta gat gca 451			
Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn Arg Gln Val Asp Ala			
	105	110	115
gtg gtg cac gct cca gtt aat ccc caa gcg aag ttt cca aag ggc ttc 499			
Val Val His Ala Pro Val Asn Pro Gln Ala Lys Phe Pro Lys Gly Phe			
	120	125	130
aaa gtg gtc gag ctt aat cgt cgt agc gat ctc aac cga cct act gtg 547			
Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu Asn Arg Pro Thr Val			
	135	140	145

Asp Lys Val Leu Ala Ala Ala Glu Lys Leu Gly Tyr Arg Thr Asn Ala
 35 40 45
 Met Ala Arg Ala Leu Arg Glu Asn Lys Thr Arg Thr Val Gly Leu Ile
 50 55 60
 Val Pro Gly Ile Ile Asn Lys Phe Tyr Thr Glu Ser Ala Thr Val Leu
 65 70 75 80
 Gln Asp Glu Leu Asp Lys Ser Gly Tyr Gln Leu Val Val Ser Thr Thr
 85 90 95
 Gly Asn Asp Ala Glu Lys Glu Arg Arg Ala Ile Glu Ser Met Leu Asn
 100 105 110
 Arg Gln Val Asp Ala Val Val His Ala Pro Val Asn Pro Gln Ala Lys
 115 120 125
 Phe Pro Lys Gly Phe Lys Val Val Glu Leu Asn Arg Arg Ser Asp Leu
 130 135 140
 Asn Arg Pro Thr Val Thr Ser Asp Asp Ala Thr Gly Leu Lys Glu Leu
 145 150 155 160
 Ala Leu His Ile Leu Asp Gln Gly Tyr Arg Asp Ile Gly Ile Ile Val
 165 170 175
 Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
 180 185 190
 Asn Ala Leu Glu Thr Glu Ala Thr Gln Arg Gly Ile Arg Glu Glu Leu
 195 200 205
 Arg Phe Arg Val Val His Ser Arg Tyr Ser Pro Thr Gly Gly Tyr Glu
 210 215 220
 Ala Phe Ala Glu Phe Arg Asn Asp Leu Pro Gln Ile Val Val Pro Leu
 225 230 235 240
 Ser Thr Gln Leu Thr Leu Gly Val Leu Lys Ala Thr Gln Glu Asn Gly
 245 250 255
 Ile Lys Ile Ser Asp Asp Leu Ser Leu Ala Cys Tyr Gly Val Ala Glu
 260 265 270
 Trp Leu Ala Val Trp Gly Pro Gly Ile Thr Val Phe Ala Pro Asp Leu
 275 280 285
 Pro Ala Met Gly Ala Ala Ala Ala Thr Gln Val Leu Thr Leu Leu Asp
 290 295 300
 Ala Ala Pro Leu Pro Glu Asn His Leu Ser Ile Pro Gly Gln Leu Ile
 305 310 315 320
 Val Arg Gly Thr Thr Pro Lys Val
 325

<210> 359

<211> 759

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(759)

<223> RXS03200

<400> 359

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Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp Ala Ala Glu Ser	
1 5 10 15	
ttc ctc tcc cac gcc aag ggc gcc aac ggt tcg ctc act gga ccg ttg	96
Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu	
20 25 30	
acc gta ggc atc atc ccc acg gcg gct cct tac att ttg ccg tca atg	144
Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met	
35 40 45	
ctg tcc atc gtg gat gaa gaa tat cca gat ctg gaa cct cac atc gtc	192
Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val	
50 55 60	
gag gac caa acc aag cat ctt ctc gcg ttg ctg cgc gac ggc gcc atc	240
Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile	
65 70 75 80	
gac gtc gcc atg atg gcc ctg cct tct gag gca cca ggc atg aag gaa	288
Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu	
85 90 95	
atc ccc ctc tac gac gaa gac ttt atc gtc gtt aca gct agc gat cac	336
Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His	
100 105 110	
ccc ttc gcc ggc cgc caa gac tta gaa cta tcc gcc tta gaa gac ctc	384
Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu	
115 120 125	
gat ctg ctg ctt ctc gac gac gga cac tgc ctc cac gac caa att gtg	432
Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val	
130 135 140	
gac ctg tgc cgc cgc gga gac atc aac ccc att agc tcc act act gct	480
Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala	
145 150 155 160	
gtc acc cgc gca tcc agc ctt acc acc gtc atg cag ctc gtc gtc gcc	528
Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala	
165 170 175	
ggc ctt gga tcc acc ttg gtc cca atc agc gca atc cca tgg gaa tgc	576
Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys	
180 185 190	
acc cga cca gga ctg gca aca gcc aac ttc aac tct gat gtc acc gca	624
Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala	
195 200 205	

aac cgc cgc att gga ttg gtg tac cgt tcc tct tct tct cgc gcc gaa 672
 Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
 210 215 220

gag ttc gaa cag ttt gca ctc att ttg cag cgc gct ttc caa gaa gcc 720
 Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
 225 230 235 240

gtc gcg ctt gct gcc tca act ggc atc acc ttg aag caa 759
 Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln
 245 250

<210> 360

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Glu Lys Leu Leu Pro Phe Ala Lys Ser Thr Leu Asp Ala Ala Glu Ser
 1 5 10 15

Phe Leu Ser His Ala Lys Gly Ala Asn Gly Ser Leu Thr Gly Pro Leu
 20 25 30

Thr Val Gly Ile Ile Pro Thr Ala Ala Pro Tyr Ile Leu Pro Ser Met
 35 40 45

Leu Ser Ile Val Asp Glu Glu Tyr Pro Asp Leu Glu Pro His Ile Val
 50 55 60

Glu Asp Gln Thr Lys His Leu Leu Ala Leu Leu Arg Asp Gly Ala Ile
 65 70 75 80

Asp Val Ala Met Met Ala Leu Pro Ser Glu Ala Pro Gly Met Lys Glu
 85 90 95

Ile Pro Leu Tyr Asp Glu Asp Phe Ile Val Val Thr Ala Ser Asp His
 100 105 110

Pro Phe Ala Gly Arg Gln Asp Leu Glu Leu Ser Ala Leu Glu Asp Leu
 115 120 125

Asp Leu Leu Leu Leu Asp Asp Gly His Cys Leu His Asp Gln Ile Val
 130 135 140

Asp Leu Cys Arg Arg Gly Asp Ile Asn Pro Ile Ser Ser Thr Thr Ala
 145 150 155 160

Val Thr Arg Ala Ser Ser Leu Thr Thr Val Met Gln Leu Val Val Ala
 165 170 175

Gly Leu Gly Ser Thr Leu Val Pro Ile Ser Ala Ile Pro Trp Glu Cys
 180 185 190

Thr Arg Pro Gly Leu Ala Thr Ala Asn Phe Asn Ser Asp Val Thr Ala
 195 200 205

Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
 210 215 220

Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
225 230 235 240

Val Ala Leu Ala Ala Ser Thr Gly Ile Thr Leu Lys Gln
245 250

<210> 361

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Primer

<400> 361

ggaaacagta tgaccatg

18

<210> 362

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Primer

<400> 362

gtaaaacgac ggccagt

17



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